

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:30:49 ; Search time 408 Seconds
(without alignments)
8971.662 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atgcttcaagatacagct.....atgcgcagtaactgttgtag 1356

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 2552756 seqs, 1349719017 residues

Total number of hits satisfying chosen parameters: 5105512

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

N Geneseq 19Jun03:*

- 1: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1980.DAT:*
- 2: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*
- 3: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*
- 4: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*
- 5: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
- 6: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
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- 21: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2000.DAT:*
- 22: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001A.DAT:*
- 23: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2001B.DAT:*
- 24: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2002.DAT:*
- 25: /SIDSL1/gcgdata/geneseq/geneseqn-emb1/NA2003.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1356	100.0	1356	21	Sequence encoding
2	1340	98.8	1605	21	F. graminearum tri
3	915.6	67.5	1403	21	Sequence encoding
4	915.6	67.5	12949	21	Transformation vec
5	915.6	67.5	13737	21	Transformation vec
6	249.8	18.4	1425	21	Sequence encoding
7	146.2	10.8	695	21	Aspergillus oryzae
8	116.2	8.6	482	25	Aspergillus oryzae

9	39.8	2.9	4403765	22	AA199683	Mycobacterium tube
10	39.8	2.9	4411529	22	AA199682	Mycobacterium tube
11	36.4	2.7	1605	17	AA137310	Aromatic acyl tran
c 12	35.6	2.6	1459	24	ABQ33692	Oligonucleotide fo
13	35.6	2.6	1459	24	ABQ33693	Oligonucleotide fo
c 14	35.6	2.6	1463	24	ABQ14442	Oligonucleotide fo
15	35.6	2.6	1463	24	ABQ14443	Oligonucleotide fo
16	35.4	2.6	34980	22	AAH41223	Pyrococcus abyssi
17	34.2	2.5	7234	23	AA574818	DNA encoding novel
18	34	2.5	369	25	ABZ40050	N. gonorrhoeae nuc
c 19	34	2.5	3115	24	ABQ43652	Oligonucleotide fo
c 20	34	2.5	3115	24	ABQ43653	Oligonucleotide fo
21	34	2.5	26223	22	AA28554	Genomic fragment #
c 22	33.8	2.5	1077	23	AA593503	DNA encoding novel
23	33.8	2.5	2899	22	AAH02926	Human shear stress
24	33.8	2.5	2955	24	ABN95650	Gene #2148 used to
25	33.8	2.5	2955	25	ABZ75899	Heart disease targ
26	33.8	2.5	3075	24	AA594880	Human DNA sequence
c 27	33.8	2.5	21567	23	AA59514	Propionibacterium
28	33.6	2.5	1737	23	ABL56857	Rice derived plant
29	33.6	2.5	1737	24	ABQ82682	Rice blight resist
30	33.4	2.5	675	22	AAH68266	C glutamicum codin
31	33.4	2.5	675	25	ACA01814	C. glutamicum deri
32	33.4	2.5	2997	18	AA293597	Emeria tenella sp
33	33.4	2.5	3094	10	AA292579	Sequence of the 1.
34	33.4	2.5	3094	18	AA293596	Emeria tenella sp
c 35	33.4	2.5	4098	23	ABL41555	Fusion gene of tre
c 36	33.4	2.5	4716	23	ABL41560	Fusion gene of tre
c 37	33.4	2.5	6977	14	AAQ35900	Polyhydroxyalkanoa
c 38	33.4	2.5	309400	22	AAH68534	C glutamicum codin
c 39	33.4	2.5	34980	24	ABQ81845	Bifidobacterium lo
c 40	33.2	2.4	701	24	ABQ17898	Oligonucleotide fo
41	33.2	2.4	701	24	ABQ17899	Oligonucleotide fo
c 42	33.2	2.4	938	24	ABQ42724	Oligonucleotide fo
c 43	33.2	2.4	938	24	ABQ42725	Oligonucleotide fo
c 44	33.2	2.4	939	24	ABQ42118	Oligonucleotide fo
45	33.2	2.4	939	24	ABQ42119	Oligonucleotide fo

ALIGNMENTS

RESULT 1
AA54209
ID AAA54209 standard; DNA; 1356 BP.
XX
AC AAA54209;
XX
XX
DT 26-FEB-2001 (first entry)
XX
DE Sequence encoding trichothecene resistance polypeptide.
XX
KW Trichothecene resistance; resistant; crop protection; mycotoxin;
KW fungus; wheat; maize; barley; rice; heterologous gene;
KW transformation; Fusarium; ds.
XX
OS Fusarium graminearum.
XX
FH Key Location/Qualifiers
CDS 1..1356
FT /*tag= a
FT /product= Trichothecene resistance polypeptide
XX
PN WC200060061-A2.
XX
PD 12-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-EF02769.
XX
PR 31-MAR-1999; 99US-0282995.
PR 11-FEB-2000; 2000US-0502852.
XX
PA (NOVS) NOVARTIS AG.

PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX Hohn TM, Peters C, Salmerson JM, Reed JN, Dawson JL;
 PI P-PSDB; AAB03935.
 DR WPI: 2000-679374/66.
 XX Plant cell for preventing mycotoxin contamination of wheat, maize,
 PT barley or rice plant, comprises heterologous polynucleotide encoding
 PT gene product expressed in cell, having trichothecene resistance
 PT activity
 XX
 XX Claim 8; Page 48-49; 62pp; English.
 PS A heterologous gene encoding a gene product which confers
 CC trichothecene resistance can be used to transform plant cells to
 CC make them resistant to fungal infection. The transformation method is
 CC useful for preventing mycotoxin contamination of a plant,
 CC particularly a crop plant such as wheat, maize, barley or rice, and
 CC for reducing and/or preventing the growth of a fungus of the genus
 CC Fusarium that produces a trichothecene, preferably comprising a C-3
 CC hydroxyl group, by growing transformed crop plants in an area which
 CC is moderate to severe fungal infestation.
 XX
 SQ Sequence 1356 BP; 319 A; 385 C; 349 G; 303 T; 0 other;
 Query Match 100.0%; Score 1356; DB 21; Length 1356;
 Best Local Similarity 100.0%; Pred. No. 0;
 Matches 1356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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 DB 1 ATGGCTTCAAGATACAGCTCGACACCTCGGCCAGCTACGAGCCTCTTTTCGATCTAC 60
 QY 61 ACCCAATCAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTGAC 120
 DB 61 ACCCAATCAGTCTCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTGTGAC 120
 QY 121 ACCTTCGAGCAAGGTCTTAAGCGCTTTCGGAAGCGTCCCATGGTGGTCGAGCCAGTTC 180
 DB 121 ACCTTCGAGCAAGGTCTTAAGCGCTTTCGGAAGCGTCCCATGGTGGTCGAGCCAGTTC 180
 QY 181 AAGCCGAGGGATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGGAGAC 240
 DB 181 AAGCCGAGGGATTAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGGAGAC 240
 QY 241 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300
 DB 241 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300
 QY 301 ATGAGAAGGGGATACCCCTATGGCGATGTTTACGAGAACATATCGCGCCCAAGGAAG 360
 DB 301 ATGAGAAGGGGATACCCCTATGGCGATGTTTACGAGAACATATCGCGCCCAAGGAAG 360
 QY 361 ACGTTACTATTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 DB 361 ACGTTACTATTGACCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420
 QY 421 CTCAACTTCATCAAGGGCGGACTCATCTCTCACTGTCGAAGACGATGATGCTGATGAT 480
 DB 421 CTCAACTTCATCAAGGGCGGACTCATCTCTCACTGTCGAAGACGATGATGCTGATGAT 480
 QY 481 ATGTTAGCCCAAGATGCGGTGATCCGCTCTACTCTCAAGGGCGTCCGATGACGCCATTC 540
 DB 481 ATGTTAGCCCAAGATGCGGTGATCCGCTCTACTCTCAAGGGCGTCCGATGACGCCATTC 540
 QY 541 ACCGAAGGAAATGACGGCCATCAACCTCGATCGCAAGACGATGATGCTTACTCTTGA 600
 DB 541 ACCGAAGGAAATGACGGCCATCAACCTCGATCGCAAGACGATGATGCTTACTCTTGA 600
 QY 601 AACTATACGATGCGCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGATGATGATGAT 660
 DB 601 AACTATACGATGCGCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGATGATGATGAT 660

RESULT 2

AAZ89368

ID AAZ89368 standard; DNA; 1605 BP.

XX

AC AAZ89368;

XX

DT 09-JUN-2000 (first entry)

XX

DE F. graminearum trichothecene 3-O-acetyltransferase DNA.

XX

XX Trichothecene 3-O-acetyltransferase; selective marker; ds.

XX

OS Fusarium graminearum.

XX

XX Location/Qualifiers

FT CDS 135..1490

FT /*tag= a

XX /product= "trichothecine 3-O-acetyltransferase"

XX

PN JP2000032985-A.

XX

XX 02-FEB-2000.

XX

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PF 15-JUL-1998; 98JP-0200280.
XX
PR 15-JUL-1998; 98JP-0200280.
XX
PA (RIKA) RIKAGAKU KENKYUSHO.
PA (YAMA/) YAWAGUCHI I.
XX
DR WPI: 2000-274037/24.
DR P-PSDB; AAY51848.
XX
PT Trichothecin 3-O-acetyltransferase gene useful as a selective marker in
PT gene manipulations in eukaryotic host cells -
XX
PS Claim 3; Page 16-18; 25pp; Japanese.
XX
CC This invention describes a novel protein with trichothecin
CC 3-O-acetyltransferase activity. The gene is used as a selective marker
CC in a gene manipulation using eukaryote as the host cell. This sequence
CC encodes the trichothecin 3-O-acetyltransferase isolated from Fusarium
CC graminearum.
XX
SQ Sequence 1605 BP; 397 A; 459 C; 393 G; 356 T; 0 other;

Query Match 98.8%; Score 1340; DB 21; Length 1605;
Best Local Similarity 99.3%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;

QY 1 ATGGCTTTCAAGATACAGCTCGACACCTCGGCGAGCTACGAGGCTCTTTTCGATAC 60
DB 135 ATGGCTTTCAAGATACAGCTCGACACCTCGGCGAGCTACGAGGCTCTTTTCGATAC 194
QY 61 ACCCAATCAGTCTCCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTTCGAC 120
DB 195 ACCCAATCAGTCTCCTTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTTCGAC 254
QY 121 ACCTTCGAGCAAGGCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGGTCCGAGGCCAGGTC 180
DB 255 ACCTTCGAGCAAGGCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGGTCCGAGGCCAGGTC 314
QY 181 AAAGCGGAGGCTTTAGCGAGGAAACACAGAACTTCTCTTATGTCCTCTTTTGGAGAC 240
DB 315 AAAGCGGAGGCTTTAGCGAGGAAACACAGAACTTCTCTTATGTCCTCTTTTGGAGAC 374
QY 241 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 300
DB 375 GTTCTCTGTGTGTAGTGAAGACCTCCGCGATGATCCTTCAGCGCCACGATCGAGGT 434
QY 301 ATGAGAAAGCGGGATACCTTATGGCGATGTTTCAAGAGAACATCATCGCGCCAGGAAG 360
DB 435 ATGAGAAAGCGGGATACCTTATGGCGATGTTTCAAGAGAACATCATCGCGCCAGGAAG 494
QY 361 ACCTTACCTATTGACCTGTACTGTTCGCGAGACCCAAAGCCTGTAAATTCTATTGAG 420
DB 495 ACCTTACCTATTGACCTGTACTGTTCGCGCCAGCAGCACCAGCCTGTAAATTCTATTGAG 554
QY 421 CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGACAGCGGTGCTATGGAT 480
DB 555 CTCAACTTCATCAAGGCGGACTCATCTCTCACTGTCAACGACAGCGGTGCTATGGAT 614
QY 481 ATGTTAGGCCAAGATGCGGTGATCCGCTTACTCTCCAAGGCGTGCCTGTAAAGCCCATTC 540
DB 615 ATGTTAGGCCAAGATGCGGTGATCCGCTTACTCTCCAAGGCGTGCCTGTAAAGCCCATTC 674
QY 541 ACCGAAGAGGAATGACGGCCATGAACCTCGATCGAAGACGATGTTCTTACCTTCAA 600
DB 675 ACCGAAGAGGAATGACGGCCATGAACCTCGATCGAAGACGATGTTCTTACCTTCAA 734
QY 601 AACTATACGATTGGCCCGAGTAGATCATCAGATTGTCAAGCTGATGCTGTGGT 660
DB 735 AACTATACGATTGGCCCGAGTAGATCATCAGATTGTCAAGCTGATGCTGTGGT 794
QY 661 GACGCTGTCTCAGCGCGGTGAGTGCAGCTGGCGTCTTTCATCATTCAGGCCCAAGGCC 720
DB 795 GACGCTGTCTCAGCGCGGTGAGTGCAGCTGGCGTCTTTCATCATTCAGGCCCAAGGCC 854
QY 721 ATGTCAAGAGCTCAAGGATGCTCTTACCAAGACTCTTTGACGCTACCAAAAGTTCTGTGCG 780
DB 855 ATGTCAAGAGCTCAAGGATGCTCTTACCAAGACTCTTTGACGCTACCAAAAGTTCTGTGCG 914
QY 781 ACTGACGATGCTCTTTTCGGCGTTCATCTGGAATCGGCTCTCGGCTGCTCGAAGA 840
DB 915 ACTGACGATGCTCTTTTCGGCGTTCATCTGGAATCGGCTCTCGGCTGCTCGAAGA 974
QY 841 ATCGATGGCTTCGACCTACCGAGTTCCTGCGCTGTGTGATGCTCGACCGCAATGGGT 900
DB 975 ATCGATGGCTTCGACCTACCGAGTTCCTGCGCTGTGTGATGCTCGACCGCAATGGGT 1034
QY 901 GTCTCGAAACACTACCCAGGCTCTTCAAAACATGACCTACCAACACTCGACCATGGC 960
DB 1035 GTCTCGAAACACTACCCAGGCTCTTCAAAACATGACCTACCAACACTCGACCATGGC 1094
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DB 1155 CGGACATGCGCGCAAGCAAGAGTCTCGCGAGTACCTGCAACAACTCGACCATGGC 1214
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DB 1215 TCCAACTGATCCCTGACGCGCTGATCGGCAACCATCTACAGCGCTCATGCTGAGTTCTTGG 1274
QY 1141 GCCAAGTGGGACTCTGGGATTCAGCTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1200
DB 1275 GCCAAGTGGGACTCTGGGATTCAGCTTGGGCTCGGACTGGGTAAAGCCGAGACTGTG 1334
QY 1201 AGACGGCCAACTCTTTGAGCCTTTGAGAGCTTGTGATGTTTATGCTTATGCTTAAAGCCGAT 1260
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DB 1395 GCGGAGTTCCTGCGGCGCTTTCTCTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGAT 1454
QY 1321 AAGAGTGGACCAAGTATGCGCATGATCGTTGGTTAG 1356
DB 1455 AAGAGTGGACCAAGTATGCGCATGATCGTTGGTTAG 1490

RESULT 3
AAAS4206
ID AAAS4206 standard; cDNA; 1403 BP.
XX
XX AAAS4206;
XX AC
XX DT 26-FEB-2001 (first entry)
XX
DE Sequence encoding trichothecin resistance polypeptide.
XX
XX Trichothecin resistance; resistant; crop protection; mycotoxin;
XX fungus; wheat; maize; barley; rice; heterologous gene;
XX transformation; Fusarium; ds.
XX
OS Fusarium sporotrichioides.
XX
XX Key Location/Qualifiers
XX CDS 7..1386
XX FT /*tag= a
XX FT /product= Trichothecin resistance polypeptide
XX
XX WO200006061-A2.
XX
XX 12-OCT-2000.
XX
XX 29-MAR-2000; 2000WO-EP02769.
XX PF
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XX 31-MAR-1999; 99US-0282995.
 PR 11-FEB-2000; 2000US-0502852.
 XX
 XX (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-BEFINDUNGEN VERW GES MBH.
 XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
 PI P-PSDB; AAB03934.
 DR WPI; 2000-679374/66.
 XX
 XX Plant cell for preventing mycotoxin contamination of wheat, maize,
 PT barley or rice plant, comprises heterologous polynucleotide encoding
 PT gene product expressed in cell, having trichothecene resistance
 PT activity
 XX
 XX Claim 8; Page 46; 62pp; English.
 PS
 XX A heterologous gene encoding a gene product which confers
 CC trichothecene resistance can be used to transform plant cells to
 CC make them resistant to fungal infection. The transformation method is
 CC useful for preventing mycotoxin contamination of a plant,
 CC particularly a crop plant such as wheat, maize, barley or rice, and
 CC for reducing and/or preventing the growth of a fungus of the genus
 CC Fusarium that produces a trichothecene, preferably comprising a C-3
 CC hydroxyl group, by growing transformed crop plants in an area which
 CC is moderate to severe fungal infestation.
 XX
 SQ Sequence 1403 BP; 350 A; 397 C; 352 G; 304 T; 0 other;
 Query Match 67.5%; Score 915.6; DB 21; Length 1403;
 Best Local Similarity 80.3%; Pred. No. 6.2e-281;
 Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
 QY 3 GGCTTTCAAGATACAGTCTGACACCCCTCGGCCAGCTACACAGGCTCCTTTGATCTACAC 62
 DB 36 GTCTTTGACATAGAGTCTGACATCATCGGCCAGCACCGCTCTTTTCAATCTACAC 95
 QY 63 CCAAACTAGTCTCTTACCCGCTCTGATCTCTCAATATCCCACTATTGTGACAC 122
 DB 96 CCAGATCAGTCTCGTTTACCCGCTCTGATCTCTCCAGTATCCCACTATCGTCGACAC 155
 QY 123 CTTGAGCAGGCTTTAGCGCTTCTCGAGCGCTCCCATGGTTCGAGCCAGGCA 182
 DB 156 CCTTGAGGAGGCTTAAACGCCCTCTCTCAAACTTCCCATGGTTCGAGCCAGGCA 215
 QY 183 AGCGAGGCTATTAGCGAGGAAACACAGGAACCTTCTTTATCGTCCCTTTTGAGGACGT 242
 DB 216 GACCGAGGCTATGCGAGGAAACACAGGAACCTTCCAGACTTCCATATGAGGAC 275
 QY 243 TCCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTTCAGCGCCGATCGAGGAT 302
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 QY 303 GAGAAAGCGGATACCTTATGCGATGTTTACGAGAACATCATCGGCCAAGGAGAC 362
 DB 336 GAGAAAGCGGCTTTCCTTTAGAGATGTTTGAAGAACGCTGCTGCTCCGAGGAGAC 395
 QY 363 GTTACCTATTGACCTGCTACTGCTCCGAGACCCAAAGCTTGTATTTATGACGT 422
 DB 396 ATTAGCTATTGACCTGCTGCTGCTCCGAGACCCGAGGCTGTTGCTATTGACGT 455
 QY 423 CAATCTATCAAGGCGGACCTATCTCTCATCTGTGCAACGAGACGCTGCTATGATAT 482
 DB 456 CAATCTTATTAAAGCGGACCTCAITCTCACCGTCAACGAGCAACATGCTGCTATGACAT 515
 QY 483 GGTAGGCCAAGATCGGATGCTCGCTACTCTCCAAAGCGCTGCGTAAACGACCACTTCC 542
 DB 516 GACAGGCAAGATGCAATATTTCGCTCTCTCCAGGCGTCCGCAACGATCATCTTCC 575
 QY 543 CGAAGAGGAAATGACGGGCAATGAACCTCGATCGCAAGACGATGTTCTTACTCTTGA 602

DB 576 CGAGGAGGAAATCTCGGCCATGAACTCGATCGAAGCGGTAGTCCCTCTCTTGA 635
 QY 603 CTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGGTGA 662
 DB 636 CTACAAAGTTGGTCTGAGCTAGACCAACAGATCGCCAAACC---TGGCCTGTGCGGA 692
 QY 663 CGCTGTTCTCACGCCGCTCAGTGCAAGCTGGGGTCTTTCATCTCAGCCCCAAGCCAT 722
 DB 693 CGCTCCACCCGACCGGCCAAGCAAGCTGGGGTCTTCTTTCATCTCACTCCCAAGCCCT 752
 QY 723 GTCAGAGCTCAAGGATGCTCTACCAAGACTCTTGACGATCAACAAAGTCTGCTGAC 782
 DB 753 CTCGGAGCTGAAGAGCGCAGCACAAGAACTCTTGACGCTGCTCAGTTTGTGTCAAC 812
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 DB 813 TGATGATGCTCTTTGGGCTTCTCATCTGCAATCAACCTCGCGCTAGCTCTGCAAGAT 872
 QY 843 CGATGGCTCTGCACCTACCGAGTCTGCGGCTGCTGTGATGCTCGACCGCAATGGTGT 902
 DB 873 GGATGCTTCCACACCTACTGAACTTCTGCGCGCTGTCGACATCGGGGGCCCAATGGCGT 932
 QY 903 CTCGAACAATACCCAGGCTTCTTCAAAACATGACTACCAACTCGACCACTCGGCGA 962
 DB 933 ATCAAGCACATACCCAGGCTTCTTCAAAACATGACTACCAACTCGACCGCTCGCGA 992
 QY 963 AATCGCAACGAGTCTACTCGCGCAACAGCATCACGCTTCTGTTTCAAACTCGACCCCGC 1022
 DB 993 AATCGCAACGAACTTGGCGCAACAGCATCACGCTTGGCTCGGAACCTCAACAGTGA 1052
 QY 1023 GAGCATGCGCCAGCAAGAGGTCTGCGAGTCTGCTGCTGCTGCAACCAACCCGCAAGTC 1082
 DB 1053 TCGTTTGGCGAGACGAACAACAGCTTTGGCGAGTATACATGCATGGCTGCTGCAAGTC 1112
 QY 1083 CAAGTATCTCTACCGCTGATCGGACCCATCTACAGCGTCTGCTGAGTTCTTGGGC 1142
 DB 1113 GAGCGTCTCCCTGACCGCGATCGAATCCGTCAAGCGCATCATGCTGAGTTCTTGGGC 1172
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 DB 1293 GGAGTTTACCGCGTCCATTTCTCTGAGGATGAGATATGAGAGACTAAGAGCGGATGA 1352
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 DB 1353 GGAGTGACCAAGTATCGCAGTATTTGGTTAG 1386
 RESULT 4
 AAA54213
 ID AAA54213 standard; DNA; 12949 BP.
 XX
 AC AAA54213;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Transformation vector pNOV1704.
 XX
 KW Tricothecene resistance; resistant; crop protection; mycotoxin;
 KW fungus; wheat; maize; barley; rice; heterologous gene;
 KW transformation; Fusarium; ds.
 OS Synthetic.
 XX
 PN WO2000060061-A2.
 XX

PD 12-OCT-2000.
 XX
 PF 29-MAR-2000; 2000WO-EP02769.
 XX
 PR 31-MAR-1999; 99US-0282995.
 PR 11-FEB-2000; 2000US-0502852.
 XX
 PA (NOVS) NOVARTIS AG.
 PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
 XX
 PI Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
 XX WPI; 2000-679374/66.
 DR
 PT Plant cell for preventing mycotoxin contamination of wheat, maize,
 PT barley or rice plant, comprises heterologous polynucleotide encoding
 PT gene product expressed in cell, having trichothecene resistance
 PT activity
 XX
 PS Disclosure; Page 58-62; 62pp; English.
 XX
 CC A heterologous gene encoding a gene product which confers
 CC trichothecene resistance can be used to transform plant cells to
 CC make them resistant to fungal infection. The transformation method is
 CC useful for preventing mycotoxin contamination of a plant.
 CC particularly a crop plant such as wheat, maize, barley or rice, and
 CC for reducing and/or preventing the growth of a fungus of the genus
 CC Fusarium that produces a trichothecene, preferably comprising a C-3
 CC hydroxyl group, by growing transformed crop plants in an area which
 CC is moderate to severe fungal infestation. Plasmid pNOV1704
 CC comprises the Zea mays ubiquitin promoter, the phosphate mannose
 CC isomerase selectable marker and the nopaline synthase
 CC termination sequence. pNOV1704 further comprises the Zea mays
 CC ubiquitin promoter operably linked to the trichothecene 3-O-acetyl
 CC transferase sequence given in GENESEQ record AA54206 and the nos
 CC termination sequence.
 XX
 SQ Sequence 12949 BP; 3194 A; 3146 C; 3143 G; 3466 T; 0 other;
 Query Match 67.5%; Score 915.6; DB 21; Length 12949;
 Best Local Similarity 80.3%; Pred. No. 2.1e-280;
 Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
 3 GGCTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACCGGCTCTTTCGATCTACAC 62
 11281 GTCTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCCCTCTCTTCAATCTACAC 11340
 63 CCAATCAGTCTCTCTACCCCGTCTCTGATCTCTCAATATCCCACTATTGTGAGCAC 122
 11341 CCAGATCAGTCTGTTTACCCCGTCTCTGATCTCTCCAGTATCCGACCATCGTACGAC 11400
 123 CTTTCGACCAAGGCTTAAGCGCTTCTCGGAAGCGCTCCCAATGGGTGCGAGCCAGGTCAA 182
 11401 CTTTGAGGAGGGCTAAAGCGCTCTCTCAAACTTCCCATGGGTGCGGCGCCAGGTCAA 11460
 183 AGCCGAGGCGATTAGCGAGGGAACACAGAGACTTCTTATCGTCCCTTTTGAAGAGCT 242
 11461 GACCGAGGCGATCGCGAAGGAAACACAGGAACCTTCAAGATCATTCATATGAGGAGAC 11520
 243 TCCTCGTGTGTGATGAAAGACCTTCCCGGATGATCTTCAGCGCCACGATCCAGGGGTAT 302
 11521 ACCCGCTGTGTGAAAGACCTTCCGTGATGATCTTCAGCGCCACGATCCAGGGGTT 11580
 303 GAGAAAGCGGGATACCTATGCGATGTTTGAAGAGACATCATCGCGCAAGAGAGAC 362
 11581 GAGAAAGCGGGTTTCCCTTAGAGATGTTTGAAGAGAACTGCTGCTCGGAGGAGAC 11640
 363 GTTACCTATTGAGGACTGTGTCGCGAGGACCCAAAGCGCTGTAATCTATTGCGAGCT 422
 11641 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCCGAAGCCTGTGTGCTATTGCACT 11700
 423 CAATCTCATCAAGGCGGAGCTCATCTCTCACTGTCAACGAGCAGCAACGCTCTATGATAT 482

Db	11701	CAACTTCATTAAAGGGCGAGCTCAATCTCAACCGTCAACGGAACAATGGTGTATGGACAT	11760
QY	483	GGTAGCCCAAGATGCGGTGATCCCGTCTACTCTCCAAAGCGTCCCGTAACGACCCATTTCAC	542
Db	11761	GACAGGACAAGATGCAATTAATTCGTCTCTCTCCAAAGCGTCCCGCAAGATCAATTCAC	11820
QY	543	CGAGAGGAATGACGGGCATGAACCTCGATCGCAAGACGATAGTTCTTACTTCTTAACTTAA	602
Db	11821	CGAGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGATAGTTCTTCTCTCTTCTTCTT	11880
QY	603	CTATACGATTGCGCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGCTGGTGTGA	662
Db	11881	CTACAAAGTTGCTCTGAGCTAGACCACAGATCCCAACCC---TGGCCCTGTCTGGGGA	11937
QY	663	CGCTGTTCTCAACCGCGGTCAAGTGGGCGTCTTCTTCAATTCAGCCCCCAAGGCCAT	722
Db	11938	CGCTCCACCGCACCGGCCAAGCAAGCTGGGCGTCTTCTTTCATTCATCTCCCAAGCCCT	11997
QY	723	GTACAGCTCAAGGATGCTCTCAAGACTCTTGAACGATCAACAAAGTTGGTGTGCAC	782
Db	11998	CTCGAGCTGAAAGACGCGACCAAAAGACTCTTGACCGTCTGTCAAAGTTGTGTCAAC	12057
QY	783	TGACGATGCTCTTTCGGGTTTCACTGGAATCGGCTCTCGCTGCTCGGCGCCCAATGGGCT	842
Db	12058	TGATGATGCTCTTTCGGGTTTATCTTGCAATCAACCTCGCGGTACGCTCTCGCAAGAT	12117
QY	843	CGATGGCTCTGACACTACCGAGTTCTGCGGTGCTGTGATGCTCGACCGCAATGGGCT	902
Db	12118	GGATGTTCCACACCTACTGAATTTCTGCGGCTGTGACATGCGGCGCCCAATGGGCT	12177
QY	903	CTCGAACAATCAACCGGCTCTTCAAAATGACCTTACCAATCAACATCGACATCGCGCA	962
Db	12178	ATCAAGCACATACCCAGGCTCTTCTTCAAAATGACCTTACCAATCAACATCGACATCG	12237
QY	963	AATCGCAACGAGTCACTCGCGCAACAGCATCAAGCTTCTGTTTCAGAACTCGACCCCGC	1022
Db	12238	AATCGCAACGAGTCACTCGCGCAACAGCATCAAGCTTCTGTTTCAGAACTCGACCCCGC	12297
QY	1023	GAGCATGCGCCAGCAACAAGAGTCTCGGACGCTCTGCAACAACCAACCCCGCAAGTC	1082
Db	12298	TCGTTTGGCAGACGAACAAGCTTTGGCGACGCTACATGATGCGCTGCTGCAAGTC	12357
QY	1083	CAAGTATCCCTGACGCTGATCGGACCCATCTACAGCGCTGATGCTGAGTTCTTGGGC	1142
Db	12358	GAGCTCTCCCTGACCGCGATCGAATCCGTCAAGCAGCATCATGCTGAGTTCTTGGGC	12417
QY	1143	CAAGTGGGACTCTGGGATACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG	1202
Db	12418	CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGGTAAGCCCTGAGAGTGTGAG	12477
QY	1203	ACGCCCAATCTTTGAGCTCTGAGAGCTTTGATGTACTTTATGCCCAAGAGCCCTGATGG	1262
Db	12478	AAGACCTCGCTTGAACCTTTGAGAGTTTGAAGTACTTTATGCCCAAGAGCCCTGATGG	12537
QY	1263	CGAGTCTGTGGCGCTTTCTCTGAGGATGAGGATATGAGCGATGGAAGGCGGATAA	1322
Db	12538	GGAGTTTACGCGCTCCATTTCTCTGAGGATGAGGATATGAGGAGACTAAAGGCGGATGA	12597
QY	1323	GGAGTGACCAAGTATGCGGAGTACCTTGGTTAG 1356	
Db	12598	GGAGTGACCAAGTATGCGCAAAAGTATATTTGGTTAG 12631	

RESULT 5
 AA54212
 ID AA54212 standard; DNA; 13737 BP.
 XX
 AC AA54212;
 XX
 DT 26-FEB-2001 (first entry)
 XX
 DE Transformation vector pAgroTRir.
 XX

KW Tricothecene resistance; resistant; crop protection; mycotoxin;
 KW fungus; wheat; maize; barley; rice; heterologous gene;
 KW transformation; Fusarium; ds.

XX
OS
synthetic.

XX PN WO200060061-A2.

12-OCT-2000.

29-MAR-2000: 2000WC-EP02769.

XX 31-MAR-1999; 99US-0282995.
PR

FR II-FEB-2000, ZOOOZOOOZOOOZOOO.

XX

PA (NOVS) NOVARTIS AG:
PA (NOVS) NOVARTIS-ERF

XX PI Hohn TM, Peters C, Salmemon JM, Reed JN

DR WPI; 2000-679374/66.

PT Plant cell for preve

PT gene product expressed in cell, having trichothecene resistance activity

PS Disclosure; Page 54-58; 62pp; English.

A heterologous gene encoding a gene product which confers trichothecene resistance can be used to transform plant cells to make them resistant to fungal infection. The transformation method is useful for preventing mycotoxin contamination of a plant, particularly a crop plant such as wheat, maize, barley or rice, and for reducing and/or preventing the growth of a fungus of the genus *Fusarium* that produces a trichothecene, preferably comprising a C-3 hydroxyl group, by growing transformed crop plants in an area which is moderate to severe fungal infestation. Plasmid pAgroTRIR comprises a selectable marker operably linked to a promoter and terminator sequence and the trichothecene resistance gene described in GENSEQ record AAAS4206 behind and in frame with the Arabidopsis thaliana YBI 3 promoter and in front of and in frame with the nos polyadenylation signal.

XX
SQ Sequence 13737 BP; 3341 A; 3442 C; 3629 G; 3325 T; 0 other;

Query Match	67.5%;	Score 915.6;	DB 21;	Length 13737;
Best Local Similarity	80.3%;	Pred. No. 2.1e-280;		
Matches 1087;	Conservative	0;	Mismatches 264;	Indels 3;
				Gaps 1;

Qy	3	GGCTTTCAAGATACAGCTCGACACCGCTGGCGCAGCTACGAGGCCTCCTTTGATCTACAC	62
Db	50	GTCTTTGACATAGAGCTCGACATCATCGGCAGCAACCGCGCTCTCTTTCAATCTACAC	109
Qy	63	CCAAATCAGTCTCCTTACCGCGTCTCTGATTCCTCAATATCCCATATTGTGTCAGCAC	122
Db	110	CCAGATCAGTCTCTGTTTACCCGCTCTCTGATCCCTCCAGTATCCACCATCGTCAGCAC	169
Qy	123	CTTTCGAGCAAGGTCTTTAAGCGCTTCTCCGAAGCGGTGCCATGGTTCGACGGCCAGGTCAA	182
Db	170	CCTTGAGGAAGCGCTAAACAGCGCTCTCTCAAACTTCCCATGGTTCGGGGCGAGTCAA	229
Qy	183	AGCCGAGGGCATTTAGCGAGGGAAACAACAGGAACCTTCCTTTATCTGTCCTCTTTTGAGGACGT	242
Db	230	GACCGAGGGCATCAGCGAAGGAAACAACAGGAACCTTCCAAGATCATTCCTATATGAGGAGAC	289
Qy	243	TCCTCGTGTGTAGTGAAGAAGACCTTCGCGATGATCTTTCAGCGCCCAACATCGAGGGTAT	302
Db	290	ACCCCGCTTGTGGTGAAGACCTCCGTGATGATTCCTCAGCGCCCAACGATCGAGGGGTT	349
Qy	303	GAGAAAGCGGGGATACCTCATGTCGGATGTTTGACAGGAACATCATCGCCCAAGGAAGAC	362
Db	350	GAGAAAGCGGGTTCCCTTTAGAGATGTTTGACAGGAACGTCGTGGCTCCGAGGAAGAC	409

PR 24-JUN-1998; 98US-0103840.
 XX (GENO-) INST GENOMIC RES.
 PA Fleischmann RD, White OR, Fraser CM, Venter JC;
 XX WPI; 2001-647261/74.
 XX
 DR Evaluating strain variation of Mycobacterium tuberculosis, comprises
 PT determining the nucleotide sequence of the strain at positions in the
 PT genome corresponding to positions where M. tuberculosis strains CDC
 PT 1551 and H37Rv differ
 XX
 XX Claim 3; SEQ ID NO 1; 3pp + Sequence Listing; English.
 XX
 XX The invention relates to evaluating strain variation within and between
 CC different populations of the tuberculosis bacterial pathogen,
 CC Mycobacterium tuberculosis or related Mycobacterium by determining the
 CC nucleotide sequence of the first strain at positions in the complete
 CC sequence of the genome that correspond to positions that differ in the
 CC nucleotide sequences of M. tuberculosis strains CDC 1551 (AAI99683) and
 CC H37Rv (AAI99682). The method is useful for evaluating strain variation of
 CC M. tuberculosis and has valuable application in the fields of
 CC tuberculosis genetics, epidemiology, patient treatment and epidemic
 CC monitoring.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from USPTO
 CC at seqdata.uspto.gov/sequence.html?docID=629432851.
 XX
 XX Sequence 4411529 BP; 758565 A; 1449983 C; 1444602 G; 759379 T; 0 other;
 SQ
 Query Match 2.9%; Score 39.8; DB 22; Length 4411529;
 Best Local Similarity 49.8%; Pred. No. 8.4;
 Matches 101; Conservative 0; Mismatches 102; Indels 0; Gaps 0;
 QY 956 TCGGCGAATCGCAACAGTCACTCGGCGCAACAGCATCACGCTTCGTTCAAGATCG 1015
 DB 4227170 TCGAGAGGTTCGGCGGCCCACTCGAAGAGCAGCGCAATCGCTACGGATATCC 4227229
 QY 1016 ACCCGCGAGTGGCGGACGACAGAGGTCTCGGAGCTACTCTCAACACACCCCG 1075
 DB 4227230 ACGCCACAGATCCGCGAACTCGAAGATGTCTGCGCCCGGAACCTCGGAGGAGCTCG 4227289
 QY 1076 ACGAGTCCACGTATCCCTGACGCTCATGCGGACCATCTAACAGGCTCATGCTGAGTT 1135
 DB 4227290 ACCGGTTACCTCGCGTTCAAGAGACCGCGTGGCTCGGACCGAGTGGCGATTG 4227349
 QY 1136 CTTGGGCAAGTGGGACTCTGG 1158
 DB 4227350 CCCAGGCACAGCTGGTGGCTGG 4227372
 RESULT 11
 AAT37310
 ID AAT37310 standard; cDNA to mRNA; 1605 BP.
 XX AAT37310;
 XX
 XX 06-FEB-1997 (first entry)
 XX
 XX Aromatic acyl transferase coding sequence.
 XX
 XX Aromatic acyl transferase; transformation; anthocyanin pigment;
 KW plants; acylation; colour; tone; colouration; colour change;
 KW Gentiana triflora; Petunia hybrida; Perilla ochroides;
 KW Scenecio cruentus; Lavandula angustifolia; ds.
 XX
 XX Petunia hybrida (Clone pPAT48).
 XX
 XX Key Location/Qualifiers
 FH 67..1413
 FT CDS /*tag= a
 FT /product= Aromatic acyl transferase.

XX WO9625500-A1.
 XX
 PD 22-AUG-1996.
 XX
 XX 16-FEB-1996; 96WO-JP00348.
 XX
 XX 30-JAN-1996; 96JP-0046534.
 PR 17-FEB-1995; 95JP-0067159.
 PR 29-JUN-1995; 95JP-0196915.
 XX
 XX (SUNR) SUNTORY LTD.
 XX
 XX Ashikari T, Fujiwara H, Fukui Y, Kusumi T, Mizutani M;
 PI Nakao M, Tanaka Y, Yonekura K;
 XX
 XX WPI; 1996-393401/39.
 DR P-PSDB; AAM04724.
 XX
 XX DNA coding for aromatic acyl transferase - for transforming plants
 PT which produce anthocyanin pigments and thus altering colour tone,
 PT e.g. of flowers
 XX
 XX Claim 4; Page 61-65; 94pp; Japanese.
 XX
 XX Vectors containing DNA fragments encoding proteins of plant origin
 CC with aromatic acyl transferase activity may be used to transform
 CC plants which produce anthocyanin pigments. The aromatic acyl
 CC transferase acylates the pigments in the flower resulting in colour
 CC tone changes and allowing new colourations to be produced. Six
 CC specific DNA sequences encoding aromatic acyl transferase from
 CC different plants are described in AAT37308-T37313.
 XX
 XX Sequence 1605 BP; 477 A; 319 C; 375 G; 434 T; 0 other;
 SQ
 Query Match 2.7%; Score 36.4; DB 17; Length 1605;
 Best Local Similarity 51.9%; Pred. No. 1.4;
 Matches 107; Conservative 0; Mismatches 96; Indels 3; Gaps 1;
 QY 1154 TCTGGGATTAACGACTTTGGCTCGGACTGGGTAAAGCCCGAGACTGTGAGAGCGGCAATCT 1213
 DB 1217 TCAAGGTTTACAGCTGATGATTTGGATGGGAAAGCCAGAGTGTGAGGAGTGTTCGA 1276
 QY 1214 TTGAGCCCTGTGAGAGCTTGATGTACTTTATGC--CCAAGAGCCTGTGAGCGGAGTTCT 1270
 DB 1277 ACAATAGTTTGTATGGAATGGTGTATTGTACCAAGGCAAAATGGAGGAAGAGCAATTG 1336
 QY 1271 GTGCGGCGCTTCTCTGAGGAGTGGATATGACCCGATTCAGCGCGGTAAGAGGTGGA 1330
 DB 1337 ATGTGGAGATTAGTTTGGAAAGCAATCTATGGAGAGTTGGAGAAAGATAAGAGTTCC 1396
 QY 1331 CCAAGTATGCGAGTACGTTGGTTAG 1356
 DB 1397 TCATGGAACCTGCTTAATTTGCTTAG 1422
 RESULT 12
 ABQ33692/c
 ID ABQ33692 standard; DNA; 1459 BP.
 XX
 XX ABQ33692;
 XX
 XX 12-JUL-2002 (first entry)
 XX
 XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 20283.
 DE Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
 KW drug; side effect; cancer; central nervous system; cardiovascular;
 KW gastrointestinal; respiratory system; single nucleotide polymorphism;
 KW SNP; cell differentiation; ds.
 XX
 XX Homo sapiens.
 OS
 XX

PN WO200218632-A2.
XX PD
XX PF 07-MAR-2002.
XX 01-SEP-2001; 2001WO-BP10074.
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC AB013410-AB034121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX SQ Sequence 1459 BP; 173 A; 200 C; 526 G; 560 T; 0 other;
Query Match 2.6%; Score 35.6; DB 24; Length 1459;
Best Local Similarity 49.0%; Pred. No. 2.4;
Matches 95; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 21 CGACACCTCGGCCAGCTTACCGAGGCTCTTTTCGATCTACACCCCAATCAGTCTCTCTA 80
Db 1108 CCAATTCGCGCCCACTCCGACCCGCTTACACCCGCGCCCGAGCAATCCCAAC 1049
Qy 81 CCCGCTCTGATTCCTCTCAATATCCCACTATTGTTCAGCACCTTCGAGCAAGTCTTAA 140
Db 1048 CACCGCGCGTAAACGACCAAAATTAATCTCTACCCGCGCTTTAAACCCGAAACGCA 989
Qy 141 GCGCTTCTCGAAGCGCTCCATGGTTCGAGGCGAGGTCAAAGCCGAGGCGATTAGCGA 200
Db 988 ACGAATCGAACACCCGAAACGCGCTTTCGCGGAATCTTAAACACGACGAATCGACGA 929
Qy 201 GGGAAACACAGGAA 214
Db 928 CCGAAAAAACGAA 915
RESULT 13
ABQ33693
ID ABQ33693 standard; DNA; 1459 BP.
XX AC ABQ33693;
XX 12-JUL-2002 (first entry)
XX

DE XX Oligonucleotide for detecting cytosine methylation SEQ ID NO 20284.
KW Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;
KW drug; side effect; cancer; central nervous system; cardiovascular;
KW gastrointestinal; respiratory system; single nucleotide polymorphism;
KW SNP; cell differentiation; ds.
OS Homo sapiens.
XX WO200218632-A2.
PN 07-MAR-2002.
XX 01-SEP-2001; 2001WO-BP10074.
XX 01-SEP-2000; 2000DE-1043826.
PR 05-SEP-2000; 2000DE-1044543.
XX (EPIC-) EPIGENOMICS AG.
XX Olek A, Piepenbrock C, Berlin K, Guetig D;
PI WPI; 2002-371829/40.
XX Determining the degree of cytosine methylation in genomic DNA, useful
PT for diagnosis and prognosis, comprises selective hybridization of
PT amplicons from chemically treated DNA -
XX Claim 12; 56pp + Sequence Listing; 56pp; German.
XX This invention describes a novel method for determining the degree of
CC methylation of a particular cytosine in a motif 5'-CpG-3', present in a
CC genomic sample of DNA. The sample is treated chemically to convert
CC cytosine (C) but not methylated C, to uracil, then part of the genomic
CC DNA that contains the target C is amplified to form a labeled amplicon.
CC The amplicon is hybridised to two classes, each with at least one
CC member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers
CC and the degree of hybridisation to both classes is determined from the
CC label on the amplicon. From the ratio of labels hybridised to the two
CC classes of oligomers, the degree of methylation is calculated. The method
CC is used: (i) for diagnosis and/or prognosis of side effects of
CC therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders
CC of the central nervous, cardiovascular, gastrointestinal and respiratory
CC systems etc., particularly by detecting mutations or single nucleotide
CC polymorphisms (SNP's); and (ii) for differentiation of cell or tissue
CC types and for investigating cell differentiation. The method allows the
CC methylation status of many C residues to be determined simultaneously.
CC AB013410-AB034121 represent genomic DNA sequences used to illustrate the
CC method for determining the degree of cytosine methylation described in
CC the disclosure of the invention.
XX SQ Sequence 1459 BP; 560 A; 526 C; 200 G; 173 T; 0 other;

Query Match 2.6%; Score 35.6; DB 24; Length 1459;
Best Local Similarity 49.0%; Pred. No. 2.4;
Matches 95; Conservative 0; Mismatches 99; Indels 0; Gaps 0;
Qy 21 CGACACCTCGGCCAGCTTACCGAGGCTCTTTTCGATCTACACCCCAATCAGTCTCTCTA 80
Db 352 CCAATTCGCGCCCACTCCGACCCGCTTACACCCGCGCCCGAGCAATCCCAAC 411
Qy 81 CCCGCTCTGATTCCTCTCAATATCCCACTATTGTTCAGCACCTTCGAGCAAGTCTTAA 140
Db 412 CACCGCGCGTAAACGACCAAAATTAATCTCTACCCGCGCTTTAAACCCGAAACGCA 471
Qy 141 GCGCTTCTCGAAGCGCTCCATGGTTCGAGGCGAGGTCAAAGCCGAGGCGATTAGCGA 200
Db 472 ACGAATCGAACACCCGAAACGCGCTTTCGCGGAATCTTAAACACGACGAATCGACGA 531
Qy 201 GGGAAACACAGGAA 214
Db 532 CCGAAAAAACGAA 545

RESULT 14	141	GGCGTTCTCCGAAGCCGTCCTCCATGGGTCCGACGCCAGGTCAAGCCGAGGCGATTAGCGA	200
ABQ14442/c			
ID	ABQ14442	standard; DNA; 1463 BP.	
XX			
AC	ABQ14442;		
XX			
DT	12-JUL-2002	(first entry)	
XX			
DE	Oligonucleotide for detecting cytosine methylation SEQ ID NO 1033.		
XX			
KW	Human; cytosine methylation; 5'-CpG-3'; uracil; cytosine; diagnosis;		
KW	drug; side effect; cancer; central nervous system; cardiovascular;		
KW	gastrointestinal; respiratory system; single nucleotide polymorphism;		
KW	SNP; cell differentiation; ds.		
XX			
OS	Homo sapiens.		
XX			
XX	WO200218632-A2.		
PN			
XX			
PD	07-MAR-2002.		
XX			
XX			
PF	01-SRP-2001; 2001WO-EP10074.		
XX			
XX			
PR	01-SRP-2000; 2000DE-1043826.		
PR	05-SRP-2000; 2000DE-1044543.		
XX			
XX	(BPIG-) EPIGENOMICS AG.		
PA			
XX			
XX	Olek A, Piepenbrock C, Berlin K, Guetig D;		
PI			
XX			
XX	WPI; 2002-371829/40.		
DR			
XX			
CC	Determining the degree of cytosine methylation in genomic DNA, useful		
CC	for diagnosis and prognosis, comprises selective hybridization of		
CC	amplicons from chemically treated DNA		
CC			
CC	Claim 12; 56pp + Sequence Listing; 56pp; German.		
XX			
XX	This invention describes a novel method for determining the degree of		
CC	methylation of a particular cytosine in a motif 5'-CpG-3', present in a		
CC	genomic sample of DNA. The sample is treated chemically to convert		
CC	cytosine (C) but not methylated C, to uracil, then part of the genomic		
CC	DNA that contains the target C is amplified to form a labeled amplicon.		
CC	The amplicon is hybridised to two classes, each with at least one		
CC	member, of oligonucleotides and/or peptide-nucleic acid (PNA) oligomers		
CC	and the degree of hybridisation to both classes is determined from the		
CC	label on the amplicon. From the ratio of labels hybridised to the two		
CC	classes of oligomers, the degree of methylation is calculated. The method		
CC	is used: (i) for diagnosis and/or prognosis of side effects of		
CC	therapeutic drugs and of a wide range of diseases, e.g. cancer, disorders		
CC	of the central nervous, cardiovascular, gastrointestinal and respiratory		
CC	systems etc., particularly by detecting mutations or single nucleotide		
CC	polymorphisms (SNP's); and (ii) for differentiation of cell or tissue		
CC	types and for investigating cell differentiation. The method allows the		
CC	methylation status of many C residues to be determined simultaneously.		
CC	ABQ13410-ABQ54121 represent genomic DNA sequences used to illustrate the		
CC	method for determining the degree of cytosine methylation described in		
CC	the disclosure of the invention.		
XX			
XX	Sequence 1463 BP; 189 A; 200 C; 521 G; 553 T; 0 other;		
XX			
XX	Query Match	2.6%;	Score 35.6; DB 24; Length 1463;
XX	Best Local Similarity	49.0%;	Pred. No. 2.4;
XX	Matches	95; Conservative	0; Mismatches 99; Indels 0; Gaps 0;
QY	21	CGACACCTCGCCAGGTACAGGCTCTTTTCGATCTTACACCCAAATCAGTCTCTCTA	80
DB	1018	CGAATTCGCGCCCACTCCGACCCCGACGTTTACACCCGCCCGCCGACGATCCCCAC	959
QY	*81	CCCCGCTCTGATTCCTCTCAATATCCCACTATTGTCAGACCTTCGAGCAAGTCTTAA	140
DB	958	CACCGCGGTAAACGACCAACAAAATAATCTCTACCCGCGGCTTTAAAAACCGAACGCA	899

	Matches	95;	Conservative	0;	Mismatches	99;	Indels	0;	Gaps	0;
Qy	21	CGACACCTTCGCGCCAGCTACGAGGCTCTTTTCGATCTACACCCAAATCAGTCTCTCTTA	80							
Db	446	CCAAATTCGCGCCAACTCCGACCCCGCGTTTACACCCCGCCCGACGAATCCGCACAC	505							
Qy	81	CCCCGTCTCTGATTCTCTCAATATCCCACTATTGTGACACCTTCGAGCAGGTCTTAA	140							
Db	506	CACCGCCGGTAAACGACCAAAATTAATCTCTACCCCGGCTTTAAACCCGAAACGCA	565							
Qy	141	GGCTTTCGGAAGCGTCCATGGTTCGAGCCAGGTCAAAGCCGAGGGCATTAGGGA	200							
Db	566	ACGAATCGAACAACCCGAAACGCGGTCTTCGCGAATCTTAAACGACGHAATCGACGA	625							
Qy	201	GGGAACACAGGAA	214							
Db	626	CGAAAAAAACGAA	639							

Search completed: February 7, 2004, 21:53:45
 Job time : 417 secs

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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 17:54:07 ; Search time 5222 Seconds
(without alignments)
10623.028 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggcttcaagatacacgt.....atgcgcagtaactgttgtag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 2888711 seqs, 20454813386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba.*

2: gb_htg.*

3: gb_in.*

4: gb_om.*

5: gb_ov.*

6: gb_pat.*

7: gb_ph.*

8: gb_pl.*

9: gb_pt.*

10: gb_ro.*

11: gb_sts.*

12: gb_sy.*

13: gb_un.*

14: gb_vi.*

15: em_ba.*

16: em_fun.*

17: em_hum.*

18: em_in.*

19: em_mu.*

20: em_om.*

21: em_or.*

22: em_ov.*

23: em_pat.*

24: em_ph.*

25: em_pl.*

26: em_ro.*

27: em_sts.*

28: em_un.*

29: em_vi.*

30: em_htg_hum.*

31: em_htg_inv.*

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33: em_htg_mus.*

34: em_htg_pln.*

35: em_htg_rod.*

36: em_htg_man.*

37: em_htg_vrt.*

38: em_sy.*

39: em_htgo_hum.*

40: em_htgo_mus.*

41: em_htgo_other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	1356	100.0	1356	6	AR193433	AR193433 Sequence
2	1340	98.8	1605	6	E31785	E31785 Trichothec
3	1340	98.8	1605	8	AB000874	AB000874 Gibberell
4	1340	98.8	3003	8	AB009607	AB009607 Gibberell
5	1340	98.8	8646	8	AB011417	AB011417 Gibberell
6	1334	98.4	1336	8	AF212605	AF212605 Gibberell
7	1334	98.4	1336	8	AF212608	AF212608 Gibberell
8	1330.8	98.1	1336	8	AF212603	AF212603 Gibberell
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10	1330.8	98.1	1336	8	AF212607	AF212607 Gibberell
11	1329.2	98.0	1336	8	AF212602	AF212602 Gibberell
12	1329.2	98.0	1336	8	AF212604	AF212604 Gibberell
13	1321.2	97.4	1336	8	AF212582	AF212582 Gibberell
14	1321.2	97.4	1336	8	AF212583	AF212583 Gibberell
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ALIGNMENTS

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LOCUS AR193433 1356 bp DNA linear PAT 20-APR-2002
DEFINITION Sequence 5 from patent US 6346655.
ACCESSION AR193433
VERSION AR193433.1 GI:20239398
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1356)
AUTHORS Hohn,T.M., Peters,C. and Salmemon,J.
TITLE Trichothecne-Resistant transgenic plants
JOURNAL Patent: US 6346655-A 5 12-FEB-2002;
FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 0;
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LOCUS Trichothecene 3-O-acetyltransferase gene.
DEFINITION E31785
ACCESSION E31785
VERSION E31785.1 GI:13018619
KEYWORDS JP 2000032985-A/1.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
REFERENCE Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
TITLE Isami, Y., Makoto, K., Akira, T., Hiroyuki, K. and Katsumi, Y.
JOURNAL Trichothecene 3-O-acetyltransferase gene
Patent: JP 2000032985-A 1 02-FEB-2000;
RIKAGAKU KENKYUSHO, ISAMU YAMAGUCHI
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PN JP 2000032985-A/1
PD 02-FEB-2000
PF 15-JUL-1998 JP 1998200280
PR ISAMU YAMAGUCHI, MAKOTO KIMURA, AKIRA TAKATSUKI, HIROYUKI
KOSHINO, PI KATSUMI YONEYAMA
PC C12N15/09, A01H5/00, A01N63/00, C12N1/21, C12N5/10, C12N9/10// PC
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PC C12N5/00, (C12N15/00, C12R1:77), (C12N5/00, C12R1:91) CC
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Best Local Similarity 99.3%; Pred. No. 0;
Matches 1346; Conservative 0; Mismatches 10; Indels 0; Gaps 0;
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AUTHORS
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MEDLINE
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AUTHORS
TITLE
JOURNAL
FEATURES
source

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AB000874.1 GI:2804249
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Gibberella zeae
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (sites)
Kimura, M., Kaneko, I., Komiyama, M., Takatsuki, A., Koshino, H.,
Yoneyama, K. and Yamaguchi, I.
Trichothecene 3-O-acetyltransferase protects both the producing
organism and transformed yeast from related mycotoxins. Cloning and
characterization of Tril101
J. Biol. Chem. 273 (3), 1654-1661 (1998)
98104153
9430709
Kimura, M.
Direct Submission
Submitted (04-FEB-1997) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hirosewa 2-1, Wako, Saitama 351-01, Japan
(E-mail: mkimura@postman.riken.go.jp, Tel: 81-048-467-9518,
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DEFINITION Gibberella zeae genes for trichothecene 3-O-acetyltransferase,
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ACCESSION AB011417
VERSION AB011417.1 GI:3724288
KEYWORDS phosphate permease; UTP-ammonia ligase; Tril101; trichothecene
3-O-acetyltransferase.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (sites)
Kimura, M., Matsumoto, G., Shingu, Y., Yoneyama, K. and Yamaguchi, I.
The mystery of the trichothecene 3-O-acetyltransferase gene.
Analysis of the region around Tril101 and characterization of its
homologue from Fusarium sporotrichioides
FEBS Lett. 435 (2-3), 163-168 (1998)
98433864
MEDLINE 9762900
PUBMED 9762900
REFERENCE 2 (bases 1 to 8646)
AUTHORS Kimura, M.
TITLE Direct Submission
JOURNAL Submitted (23-FEB-1998) Makoto Kimura, The Institute of Physical
and Chemical Research (RIKEN), Microbial Toxicology Laboratory;
Hiroawa 2-1, Wako, Saitama 351-0198, Japan
(E-mail:mkimura@postman.riken.go.jp, Tel:81-48-467-9518,
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FEATURES
Location/Qualifiers
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DEFINITION		Gibberella zeae strain NRRL28063 trichothece	
ACCESSION		3-O-acetyltransferase, partial cds.	
VERSION		AF212605	
KEYWORDS		AF212605.1 GI:12003706	
SOURCE		Gibberella zeae	
ORGANISM		Gibberella zeae	
REFERENCE		Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;	
AUTHORS		Hypocriomycetidae; Hypocreales; Nectriaceae; Gibberella.	
TITLE		1 (bases 1 to 1336)	
		O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.	
		Gene genealogies reveal global phylogeographic structure and	
		reproductive isolation among lineages of <i>Fusarium graminearum</i> , the	
		fungus causing wheat scab	
JOURNAL		Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)	
MEDLINE		20345085	
PubMed		10869425	
REFERENCE		2 (bases 1 to 1336)	
AUTHORS		O'Donnell, K.	
TITLE		Direct Submission	
JOURNAL		Submitted (08-DEC-1999) Microbial Properties Research,	
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RESULT 7
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DEFINITION Gibberella zeae strain NRRL29169 trichothecene
3-O-acetyltransferase, partial cds.
ACCESSION AF212608
VERSION    AF212608.1 GI:12003712
KEYWORDS  Gibberella zeae
SOURCE    Gibberella zeae
ORGANISM  Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
AUTHORS   O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
TITLE     Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE   20345085
PUBMED    10869425
REFERENCE 2 (bases 1 to 1336)
AUTHORS   O'Donnell, K.
TITLE     Direct Submission
JOURNAL   Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA
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RESULT 8
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DEFINITION  Gibberella zeae strain NRRL6394 trichothecene
3-O-acetyltransferase, partial cds.
ACCESSION AF212603
VERSION   AF212603.1  GI:12003702
KEYWORDS  .
SOURCE    Gibberella zeae
ORGANISM  Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
AUTHORS  O'Donnell, K., Kistler, H. C., Takke, B. K. and Casper, H. H.
TITLE     Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE   20345085
PUBMED    10869425
REFERENCE 2 (bases 1 to 1336)
AUTHORS  O'Donnell, K.
DIRECT SUBMISSION
TITLE     Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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BASE COUNT 318 a 383 c 339 g 296 t
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Query Match      98.1%; Score 1330.8; DB 8; Length 1336;
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RESULT 9
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LOCUS Gibberella zeae strain NRRL28336 trichothecene
DEFINITION 3-O-acetyltransferase, partial cds.
ACCESSION AF212606
VERSION AF212606.1 GI:12003708

KEYWORDS Gibberella zeae
SOURCE Gibberella zeae
ORGANISM Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
AUTHORS Gene genealogies reveal global phylogeographic structure and
TITLE reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab

JOURNAL Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
MEDLINE 20345085
PUBMED 10869425
REFERENCE 2 (bases 1 to 1336)
O'Donnell, K.
AUTHORS Direct Submission
TITLE Submitted (08-DEC-1999) Microbial Properties Research,
JOURNAL NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
FEATURES Location/Qualifiers

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ORIGIN
Query Match 98.1%; Score 1330.8; DB 8; Length 1336;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
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RESULT 10
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LOCUS   AF212607
DEFINITION
Gibberella zeae strain NR128439 trichothecene
3-O-acetyltransferase, partial cds.
ACCESSION
AF212607
VERSION
AF212607.1 GI:12003710
KEYWORDS
SOURCE
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ORGANISM
Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocnemycetidae; Hypocreales; Nectriaceae; Gibberella.
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1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of Fusarium graminearum, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
20345085
PUBMED 10869425
REFERENCE
2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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BASE COUNT 317 a 384 c 340 g 295 t
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Matches 1332; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

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ACCESSION
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VERSION
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KEYWORDS
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SOURCE
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  Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
  1 (bases 1 to 1336)
  O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
  Gene genealogies reveal global phylogeographic structure and
  reproductive isolation among lineages of Fusarium graminearum, the
  fungus causing wheat scab
  Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)
JOURNAL
  20345085
MEDLINE
  10869425
PUBMED
  10869425
REFERENCE
  2 (bases 1 to 1336)
  O'Donnell, K.
  Direct Submission
  Submitted (08-DEC-1999) Microbial Properties Research,
  NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
JOURNAL
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3-O-acetyltransferase, partial cds.
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VERSION
AF212604.1 GI:12003704
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Gibberella zeae
SOURCE
Gibberella zeae
ORGANISM
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE
1 (bases 1 to 1336)
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2 (bases 1 to 1336)
O'Donnell, K.
Direct Submission
Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Matches 1331; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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1 (bases 1 to 1336)
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Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USDA, 1815 N. University St., Peoria, IL 61604, USA
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Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 1336)
O'Donnell, K., Kistler, H.C., Tacke, B.K. and Casper, H.H.
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REFERENCE 2 (bases 1 to 1336)
O'Donnell, K.
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Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA
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Matches 1326; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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RESULT 15

AF212584 1336 bp DNA linear PLN 26-JUN-2001
LOCUS Gibberella zeae strain NRRL29010 trichothecene
DEFINITION 3-O-acetyltransferase, partial cds.

ACCESSION AF212584
VERSION 1
KEYWORDS AF212584.1 GI:12003664

ORGANISM

Gibberella zeae
Gibberella zeae
Bukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.

REFERENCE

AUTHORS O'Donnell, K., Kistler, H.C., Take, B.K. and Casper, H.H.
TITLE Gene genealogies reveal global phylogeographic structure and
reproductive isolation among lineages of *Fusarium graminearum*, the
fungus causing wheat scab
Proc. Natl. Acad. Sci. U.S.A. 97 (14), 7905-7910 (2000)

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (08-DEC-1999) Microbial Properties Research,
NCAUR-ARS-USA, 1815 N. University St., Peoria, IL 61604, USA

FEATURES

source

1. .1336
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/mol_type="genomic DNA"

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/product="trichothecene 3-O-acetyltransferase"

3. .>1336

/codon_start=1

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/protein_id="AAG43691.1"

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KAGYPWMPDENIIAPRKTLPIPGTGPDDPKPVLILQNFILKGLILTVNGHHGMD
MYQDAVIRLLSKACNDPTEEMTAMNLDKPIVLYENYIIGPEVDHQIVKPDVA
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BASE COUNT

316 a 384 c 340 g 296 t

ORIGIN

Query Match 97.4%; Score 1321.2; DB 8; Length 1336;

Best Local Similarity 99.4%; Pred. No. 0;

Matches 1326; Conservative 0; Mismatches 8; Indels 0; Gaps 0;

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QY 61 ACCCAATCAGTCTCTTACCCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTGACG 120

Db 62 ACCCAATCAGTCTCTTACCCCGCTCTCTGATTCCTCTCAATATCCCACTATTGTGACG 122

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Db 363 ACGTTACCTATTGGACCTGCTACTGCTCCGACGACCCCAAGGCTGCTAACTTCTATTGCGAG 422
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QY 661 GAGCGTGTCTACGCGGCTCAGTGAAGCTGGCGCTTCTTCACTATCAGCCCAAGGCC 720
Db 663 GAGCGTGTCTACGCGGCTCAGTGAAGCTGGCGCTTCTTCACTATCAGCCCAAGGCC 722
QY 721 ATGTCAGAGCTCAAGGATGCTGTCTACCAAGACTCTTGAAGCATCAACAAGTTCGTGTG 780
Db 723 ATGTCAGAGCTCAAGGATGCTGTCTACCAAGACTCTTGAAGCATCAACAAGTTCGTGTG 782
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Db 783 ACTGACGATGCTCTTTTCGCGTTTCATCTGGAATTCGCGCTCTCGCGTGGTTCGAAAGA 842
QY 841 ATCGATGGCTCTGCACCTTACCGAGTTCTGCGGTGCTGTTGATGCTCGACCGCAATGGGT 900
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QY 1021 GCGAGATGGCGCAGGAAACAGAGGTCTCGGACCTTACAGCGCTCATGCTGAGTCTTGG 1080
Db 1023 GCGAGATGGCGCAGGAAACAGAGGTCTCGGACCTTACAGCGCTCATGCTGAGTCTTGG 1082
QY 1081 TCCAAAGTATCCCTGACGCTGATGCGGACCCATCTTACAGCGCTCATGCTGAGTCTTGG 1140
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Db 1143 GCCAAGGTGGACTCTGGGATTACGACTTTGGGTTTCGACTTGGGTAAAGCCGAGACTGTG 1202
QY 1201 AGACGCGCAATCTTTGAGCGCTTGTGAGCTTGTGAGCTTGTATCTTATGCCCAGAGGCTGAT 1260

Mon Feb 9 08:28:53 2004

Db 1203 AGACGGCCAATCTTGAGCCTGTGAGAGCTTGATGTACTTTATGCCCCAAGAAGCCTGAT 1262
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QY 1321 AAGGAGTGGACCAA 1334
Db 1323 AAGGAGTGGACCAA 1336

Search completed: February 7, 2004, 20:53:19
Job time : 5224 secs

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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 7, 2004, 21:53:49 ; Search time 553 Seconds

(without alignments)
129.450 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 MAPKIQDLTGLQLRLLSIY.....EDMDLKADEKWKYQVVG 451

Scoring table: BIOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 10%

Listing first 40 summaries

Database : A Geneseq 19Jun03.*
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24: /SIDSI/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2334	100.0	451	21 AAB03935	Trichothecene resi
2	2314	99.1	451	21 AAY51848	F. graminearum tri
3	1860.5	79.7	459	21 AAB03934	Trichothecene resi
4	962.5	41.2	474	21 AAB03936	Sequence encoding
5	170.5	7.3	424	21 AAG18711	Arabidopsis thalia
6	170.5	7.3	433	21 AAG18710	Arabidopsis thalia
7	170.5	7.3	436	24 ABUS8179	Wheat stress respo
8	170.5	7.3	450	21 AAG18709	Arabidopsis thalia
9	169.5	7.3	424	21 AAG48446	Arabidopsis thalia

10	169.5	7.3	433	21	AAG48445	Arabidopsis thalia
11	169.5	7.3	433	23	AB93749	Herbicidally activ
12	169.5	7.3	449	21	AAG48444	Arabidopsis thalia
13	168.5	7.2	446	24	ABUS8173	Corn stress respon
14	161	6.9	439	24	ABUS8177	Soybean stress res
15	156.5	6.7	442	23	AB93641	Herbicidally activ
16	154.5	6.6	431	21	AAB36457	Mango alcohol acyl
17	154	6.6	428	21	AAG24209	Arabidopsis thalia
18	154	6.6	440	21	AAG24208	Arabidopsis thalia
19	151.5	6.5	448	17	AAW04724	Aromatic acyl tran
20	151.5	6.5	459	23	AB92609	Herbicidally activ
21	149.5	6.4	450	23	AB92606	Herbicidally activ
22	149	6.4	648	23	AB92608	Herbicidally activ
23	146	6.3	443	23	AB92607	Herbicidally activ
24	143	6.1	441	21	AAG46685	Arabidopsis thalia
25	143	6.1	441	23	AB93668	Arabidopsis thalia
26	143	6.1	457	21	AAG46684	Arabidopsis thalia
27	143	6.1	475	23	AB93310	Arabidopsis thalia
28	142.5	6.1	426	21	AAG37720	Arabidopsis thalia
29	142.5	6.1	426	21	AAG37735	Arabidopsis thalia
30	142.5	6.1	426	23	AB93930	Herbicidally activ
31	142.5	6.1	438	21	AAG37734	Arabidopsis thalia
32	142.5	6.1	442	21	AAG37719	Arabidopsis thalia
33	142	6.1	448	22	AAE00254	Taxus cuspidata fu
34	141.5	6.1	436	23	AB91119	Herbicidally activ
35	138.5	5.9	327	21	AAG46686	Arabidopsis thalia
36	134.5	5.8	448	21	AAG21060	Arabidopsis thalia
37	134.5	5.8	448	23	AB93980	Herbicidally activ
38	134.5	5.8	455	21	AAG21059	Arabidopsis thalia
39	134	5.7	448	15	AA47475	Polypeptide encode
40	134	5.7	448	15	AA46929	Tobacco Ant32 geno
41	132.5	5.7	313	21	AAG25750	Arabidopsis thalia
42	132.5	5.7	479	21	AAG45712	Arabidopsis thalia
43	132.5	5.7	484	21	AAG45711	Arabidopsis thalia
44	132.5	5.7	484	23	AB93588	Herbicidally activ
45	132	5.7	439	22	AAE00240	Taxus cuspidata fu

ALIGNMENTS

RESULT 1
AAB03935
ID AAB03935 standard; Protein; 451 AA.
XX AAB03935;
AC
XX
DT 26-FEB-2001 (first entry)
XX
DE Trichothecene resistance polypeptide.
XX
KW Trichothecene resistance; resistant; crop protection; mycotoxin;
KW fungus; wheat; maize; barley; rice; heterologous gene;
KW transformation; Fusarium.
XX
OS Fusarium graminearum.
XX
FN WO200060061-A2.
XX
PD 12-OCT-2000.
XX
PF 29-MAR-2000; 2000WO-EP02769.
XX
PR 31-MAR-1999; 99US-0282995.
PR 11-FEB-2000; 2000US-0502852.
XX
PA (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
PI Hohn TM, Peters C, Salmaron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
DR N-PSDE; AAA54209.
DR

XX plant cell for preventing mycotoxin contamination of wheat, maize,
PT barley or rice plant, comprises heterologous polynucleotide encoding
PT gene product expressed in cell, having trichothecene resistance
XX activity
XX
PS Claim 15; Page 49-50; 62pp; English.
XX
CC A heterologous gene encoding a gene product which confers
CC trichothecene resistance can be used to transform plant cells to
CC make them resistant to fungal infection. The transformation method is
CC useful for preventing mycotoxin contamination of a plant,
CC particularly a crop plant such as wheat, maize, barley or rice, and
CC for reducing and/or preventing the growth of a fungus of the genus
CC Fusarium that produces a trichothecene, preferably comprising a C-3
CC hydroxyl group, by growing transformed crop plants in an area which
XX is moderate to severe fungal infestation.
XX
SQ Sequence 451 AA;

Query Match 100.0%; Score 2334; DB 21; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.4e-211;
Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 61 KAEGISSEGN'TGTSFIVPEFVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMFDENI IAPRK 120

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DB 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKASRVRLEIDGSAFTEFCRAVDARPAWG 300

QY 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360
DB 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360

QY 361 SNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKKPD 420
DB 361 SNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKKPD 420

QY 421 GEFCALSLRDEDMRLKADKWKTYAQYVG 451
DB 421 GEFCALSLRDEDMRLKADKWKTYAQYVG 451

RESULT 2
AAY51848
ID AAY51848 standard; Protein; 451 AA.
XX
XX AAY51848;
AC
XX
DT 09-JUN-2000 (first entry)
XX
XX F. graminearum trichothecene 3-O-acetyltransferase protein.
DE
XX Trichothecene 3-O-acetyltransferase; selective marker.
XX
XX Fusarium graminearum.
OS
XX JP2000032985-A.
FN
XX

PD 02-FEB-2000.
XX
XX 15-JUL-1998; 98JP-0200280.
XX
XX 15-JUL-1998; 98JP-0200280.
XX
XX (RIKA) RIKAGAKU KENKYUSHO.
PA (YAMA/) YAMAGUCHI I.
XX
XX
XX WPI; 2000-274037/24.
DR N-PSDB; AAY51848.
XX
XX Trichothecin 3-O-acetyltransferase gene useful as a selective marker in
XX gene manipulations in eukaryotic host cells -
PS Claim 1a; Page 18-19; 25pp; Japanese.
XX
XX This invention describes a novel protein with trichothecin
XX 3-O-acetyltransferase activity. The gene is used as a selective marker
XX in a gene manipulation using eukaryote as the host cell. This sequence
XX represents the trichothecin 3-O-acetyltransferase isolated from
XX Fusarium graminearum.
XX
SQ Sequence 451 AA;

Query Match 99.1%; Score 2314; DB 21; Length 451;
Best Local Similarity 99.1%; Pred. No. 4.2e-209;
Matches 447; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60
DB 1 MAFKIQDITLQGLPGLLSIYTOISLLYPVSDSQYPTIVSTFEQGLKRFSEAVPWAGQV 60

QY 61 KAEGISSEGN'TGTSFIVPEFVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMFDENI IAPRK 120
DB 61 KAEGISSEGN'TGTSFIVPEFVPRVVVKDLRDDPSAPTIIEGMRKAGYPMAMFDENI IAPRK 120

QY 121 TLPIGPOTGDDPKPVILLQINFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180
DB 121 TLPIGPOTGDDPKPVILLQINFIKGGLILTVNGQHGAMDMVGQDAVIRLLSKACRNDPF 180

QY 181 TEEMTAMNLDRTKTIIVPELYENYTIIGPEVDHQIVKADVAGGDAVLTTPVSASWAFTEFSPKA 240
DB 181 TEEMTAMNLDRTKTIIVPELYENYTIIGPEVDHQIVKADVAGGDAVLTTPVSASWAFTEFSPKA 240

QY 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKASRVRLEIDGSAFTEFCRAVDARPAWG 300
DB 241 MSELKDAATKTLDASTKFSVSTDALSAFIWKASRVRLEIDGSAFTEFCRAVDARPAWG 300

QY 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360
DB 301 VSNYPGLLQNMVTHNSTIGEIANESLGATASRLRSELDPASMRQRTGLATYLHNNDPK 360

QY 361 SNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKKPD 420
DB 361 SNVSLTADAPSTSVMLSSWAKVGLWDYDFGLGKGPETVRRPIFEFVESLMYFMPKKPD 420

QY 421 GEFCALSLRDEDMRLKADKWKTYAQYVG 451
DB 421 GEFCALSLRDEDMRLKADKWKTYAQYVG 451

RESULT 3
AAB03934
ID AAB03934 standard; Protein; 459 AA.
XX
XX AAB03934;
AC
XX
DT 26-FEB-2001 (first entry)
XX
XX Trichothecene resistance polypeptide.
DE
XX Trichothecene resistance; resistant; crop protection; mycotoxin;
KW

KW fungus; wheat; maize; barley; rice; heterologous gene;
KW transformation; Fusarium.
XX Fusarium sporotrichioides.
OS WO200060061-A2.
XX 12-OCT-2000.
XX 29-MAR-2000; 2000WO-EP02769.
XX 31-MAR-1999; 99US-0282995.
XX 11-FEB-2000; 2000US-0502852.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
XX N-PSDB; AAA54206.
XX Plant cell for preventing mycotoxin contamination of wheat, maize,
XX barley or rice plant, comprises heterologous polynucleotide encoding
XX gene product expressed in cell, having trichothecene resistance
XX activity
XX Claim 15; Page 46-48; 62pp; English.
XX A heterologous gene encoding a gene product which confers
XX trichothecene resistance can be used to transform plant cells to
XX make them resistant to fungal infection. The transformation method is
XX useful for preventing mycotoxin contamination of a plant,
XX particularly a crop plant such as wheat, maize, barley or rice, and
XX for reducing and/or preventing the growth of a fungus of the genus
XX Fusarium that produces a trichothecene, preferably comprising a C-3
XX hydroxyl group, by growing transformed crop plants in an area which
XX is moderate to severe fungal infestation.
XX Sequence 459 AA;
Query Match 79.7%; Score 1860.5; DB 21; Length 459;
Best Local Similarity 77.6%; Pred. No. 2.4e-166;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
QY 2 AFKIQDITGQLPGLLSIYTIQISLLYPVSDSQYPTIYSTFEQGLKRFSEAVPWVAGQVK 61
DB 11 SFDIELDIIGQOPPLLSIYTIQISLLYPVSDSQYPTIYSTFEQGLKRLSQTFFPWVAGQVK 70
QY 62 AEGISEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPRKT 121
DB 71 TEGISEGNTGTSKIIPYEETPLRVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPRKT 130
QY 122 LPIGFGTGDPPDKPVLILQLNFIKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPPT 181
DB 131 LAIGFGNGPNDPKPVLILQLNFIKGLLITVNGQHGAMDMTGQDAIIRLLSKACRNEST 190
QY 182 EEMTAMNLDRTKIIPYILENTYIGPEVDHQIKADVAGDAVLTPVSAWAFPTSPKAM 241
DB 191 EEEISAMNLDRTKIIPYILENTYIGPEVDHQIKADVAGDAVLTPVSAWAFPTSPKAL 249
QY 242 SELKDAATKTLDASTKFTVSTDDALSAFTWKSASRVRLERIDGSAFTFCRAVDARPAWGV 301
DB 250 SELKDAATKTLDASTKFTVSTDDALSAFTWQSTSRVRLARLDASTTEFCRAVDMRGPGV 309
QY 302 SNNYEGLLQNNYHNTSTIGETANESIGATSELRSELDPASMRQRTGRLATYLNNDPKS 361
DB 310 SSTYEGLLQNNYHNTSTIGETANESIGATSELRSELDPASMRQRTGRLATYLNNDPKS 369
QY 362 NVSLTADAPDSTVMSLSSWAKVGLWDYDFGLGIGKPEVTRRPIFPFVBSLMYFMPKPKDG 421
DB 370 SVSLTADANPSSIMLSWAKVGCWEYDFGGLGKPEVTRRPIFPFVBSLMYFMPKPKDG 429

QY 422 EFCALSLRDEMDRLKADKEWTKYQYVG 451
DB 430 EFTASISLRDEMDRLKADKEWTKYQYVG 459
RESULT 4
AAB03936
ID AAB03936 standard; Protein; 474 AA.
XX AAB03936;
XX 26-FEB-2001 (first entry)
XX Sequence encoding trichothecene resistance polypeptide.
XX Trichothecene resistance; resistant; crop protection; mycotoxin;
XX fungus; wheat; maize; barley; rice; heterologous gene;
XX transformation; Fusarium.
XX Saccharomyces cerevisiae.
XX WO200060061-A2.
XX 12-OCT-2000.
XX 29-MAR-2000; 2000WO-EP02769.
XX 31-MAR-1999; 99US-0282995.
XX 11-FEB-2000; 2000US-0502852.
XX (NOVS) NOVARTIS AG.
PA (NOVS) NOVARTIS-ERFINDUNGEN VERW GES MBH.
XX Hohn TM, Peters C, Salmeron JM, Reed JN, Dawson JL;
XX WPI; 2000-679374/66.
XX N-PSDB; AAA54210.
XX Plant cell for preventing mycotoxin contamination of wheat, maize,
XX barley or rice plant, comprises heterologous polynucleotide encoding
XX gene product expressed in cell, having trichothecene resistance
XX activity
XX Claim 15; Page 51-52; 62pp; English.
XX A heterologous gene encoding a gene product which confers
XX trichothecene resistance can be used to transform plant cells to
XX make them resistant to fungal infection. The transformation method is
XX useful for preventing mycotoxin contamination of a plant,
XX particularly a crop plant such as wheat, maize, barley or rice, and
XX for reducing and/or preventing the growth of a fungus of the genus
XX Fusarium that produces a trichothecene, preferably comprising a C-3
XX hydroxyl group, by growing transformed crop plants in an area which
XX is moderate to severe fungal infestation.
XX Sequence 474 AA;
Query Match 41.2%; Score 962.5; DB 21; Length 474;
Best Local Similarity 44.4%; Pred. No. 1.2e-81;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;
QY 6 QLDITGQLPGLLSIYTIQISLLYPVSDSQYPTIYSTFEQGLKRFSEAVPWVAGQVKARGI 65
DB 22 QLDITGQLPGLLSIYTIQISLLYPVSDSQYPTIYSTFEQGLKRFSEAVPWVAGQVKARGI 81
QY 66 SEGNTGTSFIVPFEDVRVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPRKT-PI 124
DB 82 DEGNTGTRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFPYMLDEKTFAPCMTINPP 140
QY 125 GFGTG-PDDPKPVLILQLNFIKGLLITVNGQHGAMDMVGQDAVIRLLSKACRNDPPT 183
DB 141 GNTIGMAKSPFVAVQANFISGGILVTIVGOHIMDITGQESINLNLKSKCHQKPFSD 200

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PR 19-APR-1999; 99US-0130077.
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PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
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Query Match 7.3%; Score 170.5; DB 21; Length 433;
Best Local Similarity 23.4%; Pred. No. 4.8e-07;
Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

QY 36 PTIVSTF--EQLKLR-FGEA-VPM--VAGQVKAEG-----ISEGNTGTSFIVPPFEDVERV 84
DB 44 PTGASNFDPQVWKALKSKALVPFPMAGLRKDDGRIEDCNAGAGLVFVW--ADTFSV 101
QY 85 VVKOLRDP--PSAPTIEGRKAGYPMAMPDENIIAPRKTLP-IGPGTGPDDPKPVILLQL 141
DB 102 I-----DDFGDPAPTL-----NL---RLIPEVDHSTGIHS-FPLLVLQV 137
QY 142 NFIIK-GGLILTVNGHGMDVQDAVIRLLSKACNRNPFTEEMTAMMLDRKTTVPVYLE 200
DB 138 TFFKCGGASLGVGMQHAADGSLHFINTWSDMAR-----GLD----- 176
QY 201 NVTIGPEVDHQTIVA-----DVAGGDAVLTPVSASWAFPTFSPKAM 241
DB 177 -LTTPPFIDRIILLRARDPPQAPHFHVYQAPSMKIPILDPKSGPENTTVSIFKLRDQL 235
QY 242 SELKDAATKTLDASTKFTVSTDDALSAFIWKSASRVRLERIDGSAPTFCRAVDA----RP 297
DB 236 VALK--AKSKEDGNTVSYSSYEMLAGHVRSVGKAR--GLPNDQETKLYIATDGRSLRP 291
QY 298 AMGVSNYPGLLONTYINSTI-----GEIANESLGATASRLRSLDPAAS 342
DB 292 QLP-----PGYFGNVIFATPLAVAGDLLSKPTWYAAGQIHDFLVRMDNDVILRSALD--- 343
QY 343 MRQRTGRGLATYLNPNPKNSVSLTADAPSTSVMLSSWAKVGLWDYDFGLGKPKETVRR 402
DB 344 -----YLEMPDLSALVRGHNTYKCNPLGHTSWRLPIYDADFGWG-----R 385
QY 403 PIFE-----PVESIMYFMFKKP-DGEFCAALSRLDEDM 434
DB 386 PIFMGPGGIPYEGLSFVLPSPINDGSLSAIALQSEHM 423

RESULT 7
ID ABU58179
XX ABU58179 standard; Protein; 436 AA.
AC ABU58179;
XX
DT 14-APR-2003 (first entry)
DE Wheat stress response protein #7.
XX
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KW Plant; EST; expressed sequence tag; stress response; drought;
KW heat; radiation; pathogen attack; grain flavour; disease resistance;
KW peptide-methionine sulfoxide reductase; DNA repair; enzyme;
KW intracellular protein transport.
XX
OS Triticum aestivum.
PN US2002152497-A1.
XX 17-OCT-2002.
XX 19-FEB-2002; 2002US-0078929.
XX 07-MAY-1999; 99US-133038P.
XX 07-MAY-1999; 99US-133042P.
XX 11-MAY-1999; 99US-133427P.
XX 11-MAY-1999; 99US-133428P.
XX 11-MAY-1999; 99US-133436P.
XX 11-MAY-1999; 99US-133437P.
XX 11-MAY-1999; 99US-133438P.
XX 04-JUN-1999; 99US-137667P.
XX 05-MAY-2000; 2000US-0566394.
XX (FALC/) FALCO S C.
XX (FAMO/) FAMODU O O.
XX (MEYE/) MEYERS B C.
XX (MIAO/) MIAO G.
XX (ODEL/) ODELL J T.
XX (RAFA/) RAFALSKI J A.
XX (THOR/) THORPE C J.
XX (SAXA/) SAKAI H.
XX (WENG/) WENG Z.
PI Falco SC, Famodu OO, Meyers BC, Miao G, Odell JT, Rafalski JA,
PI Thorpe CJ, Sakai H, Weng Z;
XX WPI: 2003-198391/19.
XX N-PSDB; ABX78350.
XX
XX New peptide-methionine sulfoxide reductase and nucleic acids, useful in
XX improving plant response to stress, engineering plants with increased
XX disease and stress resistance, or and improving/protecting grain flavor
XX
XX Claim 1; Fig 4; 205pp; English.
XX
XX The invention relates to isolated nucleic acids encoding plant stress
XX response proteins (including peptide-methionine sulfoxide
XX reductases) appearing as ABU58148-ABU58246 (or a protein 80% identical
XX to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum.
XX Also included are expression cassettes, transformed host cells,
XX transgenic plants/seeds, modulating the level of peptide-methionine
XX sulfoxide reductase in a plant and a computer system/data
XX processing system for identifying, analysing, or modelling a genetic
XX sequence. The plant nucleic acid is useful in developing strategies to
XX improve plant response to stress (e.g. drought, heat, radiation or
XX pathogen attack), engineering plants with increased disease and stress
XX resistance, manipulating DNA repair and recombination efficiency,
XX manipulating intracellular protein transport, and improving/protecting
XX grain flavour. The nucleic acids may also be used as probes or
XX amplification primers in the detection, quantitation or isolation of gene
XX transcripts, for recombinant expression of encoded polypeptides, as
XX immunogens in preparing or screening antibodies, and in sense or
XX antisense suppression of one or more genes in a host cell, tissue or
XX plant. The proteins may be used as immunogens or antigens to obtain
XX antibodies specifically immunoreactive with the protein, and in assays
XX for enzyme agonists or antagonists. The present sequence is a plant
XX stress response protein (or fragment).
XX
XX Sequence 436 AA;
XX
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Query Match 7.3%; Score 170.5; DB 24; Length 436;
Best Local Similarity 20.4%; Pred. No. 4.9e-07;

Matches	84; Conservative	61; Mismatches	158; Indels	109; Gaps	15;
QY	56	VACQVKAEGISEGN-----TGTSFIVPEDEVRVVKDLRDDPSATTIEGRMKAGYFMA	109		
Db	78	LAGELGREG-EGGRLQIDCNGEGALFVLARAPDVAGEDLFGSGYEPSPE-IRRMFVPFA	134		
QY	110	MFENIIAPKTLPIPGTGPDPKPKVILLQLNFIK-GGLILTWNQGHGAMDMVQDAVI	168		
Db	135	-----PSG-----DPCHMAMEQVTLKCGGVLTGTHIHVTMDGNGAFHI	176		
QY	169	RL-----LSKACANDPTEEMTAMNLDRTKIIVYLENYTIGPEVDHQIVKADVAG	219		
Db	177	QTWTGLARGLSGEACSPFHDTRLARSPR-----PEFEHPVYSPAYLN	224		
QY	220	GDAVLTFVSASWAFFTFSPKAMSELKDAATKTLDASTKFVSTDDALSATFK-----	271		
Db	225	G-----APRPVTRVYSVSKLLADIKSRCAPG-----VSTYGAVTAHLWRCMCVARGL	273		
QY	272	---SASRVRL-----ERIDGSAPTEFCRAVDARPAMGVSNKYPGLLQNMVTHNSTIGEIA	323		
Db	274	APGSDTLRVPANIRHRLRPQLPRQFFGNALVRDLTVK-----VGDVL	317		
QY	324	NESIGATASRLSELDPASMRQTRGLATYLNHNPKSNVSLTADADPSTVMLSWAKV	383		
Db	318	SQPLGYVADTIRKAVDHVD-DAYTRSVIDYLEVESEKGSQAARGQLMPESDLWVWSLGM	376		
QY	384	GLWDYDFGLGKPEVTRRPIFEPVESLMYFMPKPKDGEFCAALSLEDEMD	435		
Db	377	PMYDADFQWAPR-----FVAPAQMFSGTAYVTQCADRD	412		
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XX	DT	17-OCT-2000 (first entry)			
XX	DE	Arabidopsis thaliana protein fragment SEQ ID NO: 20227.			
XX	KW	Protein identification; signal transduction pathway; metabolic pathway;			
XX	KW	hybridisation assay; genetic mapping; gene expression control; promoter;			
XX	OS	termination sequence.			
XX	OS	Arabidopsis thaliana.			
XX	PN	EPI033405-A2.			
XX	PD	06-SEP-2000.			
XX	PF	25-FEB-2000; 2000EP-0301439.			
XX	PR	25-FEB-1999; 99US-0121825.			
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PR	21-OCT-1999;	99US-0160768.
PR	21-OCT-1999;	99US-0160770.
PR	21-OCT-1999;	99US-0160814.

Query Match 7.3%; Score 170.5; DB 21; Length 450;

Best Local Similarity 23.4%; Pred. No. 5.1e-07;

Matches 107; Conservative 61; Mismatches 153; Indels 137; Gaps 25;

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Db	61	PTGASNFDPQVMKEALSALVPFYPMAGRLKRDDDGRIEIDCNCAGLVFVV--ADTFSV	118
QY	85	VVKDLRDD--PSAPTIEGMRKAGYPMAMFDENIAPRKTLP-IGEGTGDPDPKPVILLQL	141
Db	119	I-----DDFGDPAPTL-----NL-----ROLIPEVDHSTGIHS-FPLLVLQV	154
QY	142	NFIK-GGLITVNGQHGAMDVGDVAVIRLLSKACRNDPFTTEEBMTAMNLRKTIIVPYLE	200
Db	155	TFKCGGASLGVGQHHADGFGSLHFINWSDMAR-----GLD-----	193
QY	201	NYTIGPEVDHOIVKA-----DVAGGDVAVLTPVSASWAPFTFSPKAM	241
Db	194	-LTIPPFIDRTLRRADPPQPAFHVEYQAPAPSMKIPLDPSKSGPENTVSIKLTDRQL	252
QY	242	SELKDAATKTLDASTKVFSTDDALSFTWKSASRVLERIDSGAPTEFCRAVDA----	297
Db	253	VALK--AKSKEDGNTVSYSYEMLAGHVWRSVGKAR--GLPNDQETKLIYATDGRSLRP	308
QY	298	AMGVSNYPGLQNNYHNSIT-----GEIANESIGATASRLSELDPAS	342
Db	309	QLP-----PGYFGNVITATPLAVAGDLLSKPTWVAGQIHDFLVRMDNVLSALD---	360
QY	343	MRQTRGLATYLNHNPKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPKETVRR	402
Db	361	-----YLEMQPDLVALRGATYKCNLTGITSVRLPIYDADFQWG-----R	402
QY	403	PIEB-----PVEISLWYEMPKKP-DGEFCAALSRLDEDM	434
Db	403	PIFMGGGIPYEGLSFVLPSPTNDGSLSVATALQSEHM	440

RESULT 9

AAG48446

ID AAG48446 standard; Protein; 424 AA.

XX AAG48446;

XX AC

XX 18-OCT-2000 (first entry)

XX Arabidopsis thaliana protein fragment SEQ ID NO: 61177.

XX Arabidopsis thaliana.

XX Protein identification; signal transduction pathway; metabolic pathway;

XX hybridisation assay; genetic mapping; gene expression control; promoter;

XX termination sequence.

XX Arabidopsis thaliana.

XX EP1033405-A2.

XX 06-SEP-2000.

XX 25-FEB-2000; 2000EP-0301439.

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PR	18-JUN-1999;	99US-0139750.	PR	27-AUG-1999;	99US-0151065.
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PR	23-JUL-1999;	99US-0145145.	PR	22-OCT-1999;	99US-0160980.
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 DB 177 LTIPFFIDRTLRLRRDPPQAFHVEYQAPASMKIPLDPSKSGPENTTVSIFKLRDQLV 236
 QY 243 ELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTFCRAVDA-----RPA 298
 DB 237 ALK--AKSKEDGNTVSYSSYEMLAGHVWRSVGKAR--GLPNDQETKLYIATDGRSRLRPQ 292
 QY 299 MGVSNYPGLLQNNYHNSTI-----GEIANESLGATASRLRSELDPASM 343
 DB 293 LP-----PGYFGNVIFTATPLAVAGDLSKPTWAAAGQIHDFLRMDNDYLSALD----- 343
 QY 344 RQRTGLATYLHNNPDKSNVSLTADADPSTVMLSSWAKVGLWDYDFGLGKPETVRRP 403
 DB 344 -----YLEMPQDLSALVRGAHTYKCPNLGITTSWVRLPIYDADFQWG-----RP 386
 QY 404 IFE-----PVESLMYFMPKKP-DGEFCAALSRLDEDM 434
 DB 387 IFMGPGGIPYEGLSFVLPSPTNDGSLVAIALQSEHM 423
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 ABB93749
 ID ABB93749 standard; Protein; 433 AA.
 AC ABB93749;
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 DT 31-MAY-2002 (first entry)
 DE Herbicidally active polypeptide SEQ ID NO 2960.
 DE Herbicidal; plant; agriculture; herbicide.
 KW Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX WO200210210-A2.
 XX 07-FEB-2002.
 XX 28-AUG-2001; 2001WO-EP09892.
 XX 28-AUG-2001; 2001WO-EP09892.
 XX (FARB) BAYER AG.
 XX Tietjen K, Weidler M;
 XX WPI; 2002-269010/31.
 XX Identifying plant target proteins for herbicidally active compounds,
 PT comprising aligning and comparing nucleic acid or amino acid sequences
 PT from plant with nucleic acid or amino acid sequences from non-plant
 PT organisms -
 XX Claim 5; SEQ ID NO 2960; 26lpp + Sequence Listing; English.
 XX The invention relates to identifying target proteins
 CC (ABB90790-ABB94016) for herbicidally active compounds, comprising
 CC aligning and comparing nucleic acid or amino acid sequences from plant
 CC with nucleic acid or amino acid sequences from non-plant organisms using
 CC suitable search parameters, where plant sequences having an E-value
 CC greater by a factor of 3 than the E-value of most similar non-plant
 CC sequences are selected. The polypeptides or nucleic acids encoding them
 CC are useful for identifying modulators. The identified modulators are
 CC useful as herbicides.
 XX Sequence 433 AA;
 SQ
 Query Match
 Best Local Similarity 23.0%; Pred. No. 6e-07;
 Matches 105; Conservative 61; Mismatches 156; Indels 135; Gaps 23;
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DB 44 PTGASNEFPDPOVMKEALSKALVPFYPMAGRLKDDDDGRIEDICGAGVLFVV--ADTFSV 101
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 DB 102 I-----DDFGDFAPTL-----NL---RQLIPEVDHSAGIHSPFLVLQVT 138
 QY 143 PIK--GGLILTVNGOHGAMVQGDVIRLISKACRNDFTEETAMMLDRKTIIVPYLEN 201
 DB 139 PFKCGGASLGVGMQHHAADGFGSLHFINTWSDMAR-----GLD----- 176
 QY 202 YTGPEVDHQIVKA-----DVAGGDAVLTPVSASWAFETSPKAMS 242
 DB 177 LTIPFFIDRTLRLRRDPPQAFHVEYQAPASMKIPLDPSKSGPENTTVSIFKLRDQLV 236
 QY 243 ELKDAATKTLDASTKFSVTDALSAFIWKSASRVRLERIDGSAPTFCRAVDA-----RPA 298
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 QY 299 MGVSNYPGLLQNNYHNSTI-----GEIANESLGATASRLRSELDPASM 343
 DB 293 LP-----PGYFGNVIFTATPLAVAGDLSKPTWAAAGQIHDFLRMDNDYLSALD----- 343
 QY 344 RQRTGLATYLHNNPDKSNVSLTADADPSTVMLSSWAKVGLWDYDFGLGKPETVRRP 403
 DB 344 -----YLEMPQDLSALVRGAHTYKCPNLGITTSWVRLPIYDADFQWG-----RP 386
 QY 404 IFE-----PVESLMYFMPKKP-DGEFCAALSRLDEDM 434
 DB 387 IFMGPGGIPYEGLSFVLPSPTNDGSLVAIALQSEHM 423
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 ID AAG48444 standard; Protein; 449 AA.
 AC AAG48444;
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 DT 18-OCT-2000 (first entry)
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 61175.
 DE Protein identification; signal transduction pathway; metabolic pathway;
 KW hybridisation assay; genetic mapping; gene expression control; promoter;
 KW termination sequence.
 XX Arabidopsis thaliana.
 OS Arabidopsis thaliana.
 XX EPI033405-A2.
 XX 06-SEP-2000.
 XX 25-FEB-2000; 2000EP-0301439.
 XX 25-FEB-1999; 99US-0121825.
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PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 16-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.

QY 137 ILLQLNFIK-GGLILTVNGHQGAMDMVGQDAVIRLLSKACRNDPFTTEEMTAMNDRKTI 195
 Db 143 IVLQVTHFKCGGVAIGVGHVADGFSGLHFINWADLCRGVPI-----AV 189
 QY 196 VYPLENTYIG-----PEVDHQIVKADVA-GGDAVLTPTSVA-----SWAPFTFGPKAM 241
 Db 190 MPFIDRSLRLRARDPPTPAYPHIEYQAPAMLSPEPQAALTSKATPTTAVAIKLSRAEL 249
 QY 242 SELKDAATKTLDASTFVSTDDALSAPFKSASRVLERIDGSAPTEFCRAVDARPMGV 301
 Db 250 VRLR-SQVFAEGAPRF-STYAVLAHVWRCSLAR--GLPADQPTKLYCATDGRQL-- 303
 QY 302 SNNYP-----GLLQNMTHNSTIGEIANESLGAT--ASRLRSELDPSMRQRTGLATYLH 355
 Db 304 ---QPLPEGYGNVIFTATPLANAGTGTAGVAEGASVQAALDRMD-DGYCSALDYLE 359
 QY 356 NNPKDSNVSLTADADPSTSVMLSSWAKVGLWYDFGLGLGKPTVRRPIFE-----PVES 410
 Db 360 LQDLALVKGATHTFRCPNLGLTSWRLPIHDADFGW-----RPVFMGPGIAYEG 411
 QY 411 LMVEMEK-KPDGFCFCAALSIRDEDMRLK 438
 Db 412 LAFVLPANRDGSLSVASLSQAEHMEKFR 440

RESULT 14

ABU58177
 ID ABU58177 standard; Protein; 439 AA.

XX AC ABU58177;

XX DT 14-APR-2003 (first entry)

XX DE Soybean stress response protein #9.

XX KW Plant; EST; expressed sequence tag; stress response; drought;
 KW heat; radiation; pathogen attack; grain flavour; disease resistance;
 KW peptide-methionine sulphoxide reductase; DNA repair; enzyme;
 KW intracellular protein transport.

XX OS Glycine max.

XX PN US2002152497-A1.

XX PD 17-OCT-2002.

XX PF 19-FEB-2002; 2002US-0078929.

XX PR 07-MAY-1999; 99US-133038P.

PR 07-MAY-1999; 99US-133042P.

PR 11-MAY-1999; 99US-133427P.

PR 11-MAY-1999; 99US-133428P.

PR 11-MAY-1999; 99US-133436P.

PR 11-MAY-1999; 99US-133437P.

PR 04-JUN-1999; 99US-137667P.

PR 05-MAY-2000; 2000US-0566394.

XX (FALC/) FALCO S C.

PA (FAMO/) FAMODU O O.

PA (MEYE/) MEYERS B C.

PA (MIAO/) MIAO G.

PA (ODEL/) ODELL J T.

PA (RAFA/) RAFALSKI J A.

PA (THOR/) THORPE C J.

PA (SAKA/) SAKAI H.

PA (WENG/) WENG Z.

PI Falco SC, Famodu OO, Meyers BC, Miao G, Odell JT, Rafalski JA;
 PI Thorpe CJ, Sakai H, Weng Z;
 XX WPI; 2003-198391/19.
 DR N-PSDB; ABX78348.

XX New peptide-methionine sulfoxide reductase and nucleic acids, useful in
 PT improving plant response to stress, engineering plants with increased
 PT disease and stress resistance, or and improving/protecting grain flavor
 PT
 XX Claim 1; Fig 4; 205pp; English.
 XX The invention relates to isolated nucleic acids encoding plant stress
 CC response proteins (including peptide-methionine sulphoxide
 CC reductases) appearing as ABU58148-ABU58246 (or a protein 80% identical
 CC to them) from Zea mays, Oryza sativa, Glycine max, or Triticum aestivum.
 CC Also included are expression cassettes, transformed host cells,
 CC transgenic plants/seeds, modulating the level of peptide-methionine
 CC sulphoxide reductase in a plant and a computer system/data
 CC processing system for identifying, analysing, or modelling a genetic
 CC sequence. The plant nucleic acid is useful in developing strategies to
 CC improve plant response to stress (e.g. drought, heat, radiation or
 CC pathogen attack), engineering plants with increased disease and stress
 CC resistance, manipulating DNA repair and recombination efficiency,
 CC manipulating intracellular protein transport, and improving/protecting
 CC grain flavour. The nucleic acids may also be used as probes or
 CC amplification primers in the detection, quantitation or isolation of gene
 CC transcripts, for recombinant expression of encoded polypeptides, as
 CC immunogens in preparing or screening antibodies, and in sense or
 CC antisense suppression of one or more genes in a host cell, tissue or
 CC plant. The proteins may be used as immunogens or antigens to obtain
 CC antibodies specifically immunoreactive with the protein, and in assays
 CC for enzyme agonists or antagonists. The present sequence is a plant
 CC stress response protein (or fragment).

XX Sequence 439 AA;

Query Match 6.9%; Score 161; DB 24; Length 439;
 Best Local Similarity 21.9%; Pred. No. 3.9e-06;
 Matches 99; Conservative 72; Mismatches 195; Indels 86; Gaps 20;
 QY 21 TQISLLYPVSDSSQYPTIVSTFRQGLKRFSEAVVAGQVKARGISEGNTGTSFIVFED 80
 Db 25 SNVDLVVP--NPHSTSVYFYPRENGVSNPFDA-----KVMKEALSK-----VLVEFYP 69
 QY 81 VPRVVVKDLRDDPSAPTI-----EGMR--KAGYPMAMFEDENIAP-----RKTILIGTGP 130
 Db 70 ---MAARLRDDDDGRVEIYCDAGVLFEAEATTAIEDFGDFSTLELRQLIIPSDYSAG 126
 QY 131 DDEPKVILLQLNFIK-GGLILTVNGHOGAMDMVGQDAVIRLLSKACRNDPTEEMTAMN 189
 Db 127 IHSYPLILVLQVTFYFKCGVSLGVMQHVVADGASGLHFINAWSDVAR-----G 174
 QY 190 LDRKTIIVPLENTYIG-----PEVDHQIVKADVA-----GGDAVLTPTSAS 230
 Db 175 LD-ISLPPFDITLLRARDPPLFVFDHIEYKPPATKTTPLQPSKPLGSDSTAVAVST- 232
 QY 231 WAFPTSPKAMSEIKDAATKTLDASTKVFSTDDALSAPFKSASRVLERIDGSAPTEFC 290
 Db 233 ---FKLTRDQLSTLKGKSR--DGNITISYSSYMLAGHVWRVSKAR--ALPDDQETKLY 285
 QY 291 RAVDARPA--GVSNMYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPSMRQRT 348
 Db 286 IATDGRARLPQPLPHGYFGNVIFTTTRIAVAGDLMSPKPTWYASRIHDALIRMD-NEYLR 344
 QY 349 GLATYLHNPNPKGNVSLTADADPSTSVMLSSWAKVGLWYDFGLGLGKPTVRRPIFE-- 406
 Db 345 SALDYLELQPLDKSLVRGAHTFRCPNLGLTSWRLPIHDADFGW-----RPIFMGP 396
 QY 407 ---PVESLMYFMPEKKP-DGEFCFCAALSIRDEM 434
 Db 397 GGAYEGLSFIIPSTNDGSLSLAIALPPEQM 428

RESULT 15

ABB93641

ID ABB93641 standard; Protein; 442 AA.


```
XX AC ABB93641;
XX DT 31-MAY-2002 (first entry)
XX DE Herbicidally active polypeptide SEQ ID NO 2852.
XX KW Herbicidal; plant; agriculture; herbicide.
XX OS Arabidopsis thaliana.
XX FN WO200210210-A2.
XX ED 07-FEB-2002.
XX 28-AUG-2001; 2001WO-EP09892.
XX 28-AUG-2001; 2001WO-EP09892.
XX (FARB ) BAYER AG.
XX Tietjen K, Weidler M;
XX WPI; 2002-269010/31.
XX Identifying plant target proteins for herbicidally active compounds,
XX comprising aligning and comparing nucleic acid or amino acid sequences
XX from plant with nucleic acid or amino acid sequences from non-plant
XX organisms -
XX Claim 5; SEQ ID NO 2852; 261pp + Sequence Listing; English.
XX
XX The invention relates to identifying target proteins
XX (ABB90790-ABB94016) for herbicidally active compounds, comprising
XX aligning and comparing nucleic acid or amino acid sequences from plant
XX with nucleic acid or amino acid sequences from non-plant organisms using
XX suitable search parameters, where plant sequences having an E-value
XX greater by a factor of 3 than the E-value of most similar non-plant
XX sequences are selected. The polypeptides or nucleic acids encoding them
XX are useful for identifying modulators. The identified modulators are
XX useful as herbicides.
XX
XX Sequence 442 AA;
XX
XX Query Match 6.7%; Score 156.5; DB 23; Length 442;
XX Best Local Similarity 21.1%; Pred. NO. 1e-05;
XX Matches 92; Conservative 68; Mismatches 174; Indels 101; Gaps 18;
XX
XX QY 4 KIQLDTLGLPGLLSIYTIQISLLY--PVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK 61
XX DB 24 KIHL-TPHDLLELFLYFQGLLPHKPDENSIIPLMASLSTALEIY---FPFAGRLVK 79
XX
XX QY 62 AEG-----ISEGNTGTGFIVPFEDVPRVVKD-LRDDPSAPTIEGRKAGYPMAMF 111
XX DB 80 VNNHEDTVSYIIDCDGLGAKFV-HAKAESITVNDVLQSHGSVPY-----FISKFF 129
XX
XX QY 112 DENTIAPRKTLPIGPGTDPDPKPVILLQLNFIRKGLLITVNGQGMAMVGDVIRLL 171
XX DB 130 PANNVQSRDALV-----SEPLLALQVTEMDKGVFISFGYNHNVADGTCFWKFFHTW 180
XX
XX QY 172 SKACRN--DPFTE-----EEMTAMNLDKRTIYVPLENTI---GPEVDHQIVKADVAGDA 222
XX DB 181 SKICLNGSDPSIQSIIVLKDWFCDGIDYFVHPVPLEMETLPRWEPSTKERV----- 230
XX
XX QY 223 VLTPVSASWAFFTSPKAMSELKDAATKTLDASTKVFSTDDALSATFWKSASRVRLERID 282
XX DB 231 -----FHLSSKNILDLKAKANNEIDTNDLKISSLOAVVAYLWLSI--IRHSGLN 277
XX
XX QY 283 GSAPTEFCRAVDARFAMG--VSNNYPGLLQNWYHNSTIGTIGIANESLGATASRL-----RS 336
XX DB 278 REEETQCNVAADMRLNPLLKKECFGNVTNATATTIVGELLDHGLGWTALQISKVRS 337
XX
XX QY 337 ELDEFA-----SMRQRTGLATYLNHNPDKNSVSLTADADPSTVMLSSWAKVGLW 386
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Db 338 ETNESYEVFAKNWVRNVRPKTSFGSRLANN-----SLIISSSPRFVEY 381
QY 387 DYDFGLGLGKPETVR 401
Db 382 EHDF--GWGKPIAAR 394

Search completed: February 7, 2004, 23:40:47
Job time : 554 secs
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OM protein - protein search, using sw model

Run on: February 7, 2004, 23:31:29 ; Search time 72 Seconds
(without alignments)
265.031 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 MAFKIQDLTGQLPGLLSIY.....EDMDRLKADKEWTKYQVVG 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 32817 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 32817

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A COMB.pep.*

2: /cgn2_6/ptodata/1/iaa/5B COMB.pep.*

3: /cgn2_6/ptodata/1/iaa/6A COMB.pep.*

4: /cgn2_6/ptodata/1/iaa/6B COMB.pep.*

5: /cgn2_6/ptodata/1/iaa/PCTUS COMB.pep.*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	2334	100.0	451	4	US-09-538-414-6
2	1860.5	79.7	459	4	US-09-538-414-2
3	962.5	41.2	474	4	US-09-538-414-8
4	142	6.1	448	3	US-09-457-046B-56
5	141.5	6.1	436	3	US-09-457-046B-62
6	134	5.7	448	1	US-08-207-904-2
7	134	5.7	448	1	US-08-207-904-17
8	132	5.7	439	3	US-09-457-046B-28
9	130.5	5.6	451	3	US-09-457-046B-69
10	126.5	5.4	435	3	US-09-457-046B-60
11	125.5	5.4	439	3	US-09-457-046B-68
12	124	5.3	445	3	US-09-457-046B-73
13	122	5.2	433	3	US-09-457-046B-67
14	121.5	5.2	306	3	US-09-457-046B-22
15	121.5	5.2	482	3	US-09-457-046B-63
16	118	5.1	450	3	US-09-457-046B-67
17	117	5.0	830	4	US-09-562-737-34
18	113	4.8	440	3	US-09-457-046B-45
19	112	4.4	441	3	US-09-457-046B-54
20	106.5	4.6	303	3	US-09-457-046B-20
21	105.5	4.5	446	3	US-09-457-046B-74
22	105.5	4.5	3724	2	US-08-804-227C-10
23	105.5	4.5	3724	2	US-08-804-198-4
24	104.5	4.5	1337	3	US-08-854-585-2
25	104.5	4.5	1337	4	US-09-447-533-2
26	104.5	4.5	1337	5	PCT-US95-05512-2
27	104	4.5	302	3	US-09-457-046B-24

ALIGNMENTS

RESULT 1

US-09-538-414-6
; Sequence 6, Application US/09538414

; Patent No. 6346655

; GENERAL INFORMATION:

; APPLICANT: Hohn, T.

; APPLICANT: Salmeron, J.

; APPLICANT: Peters, C.

; APPLICANT: Kendra, D.

; APPLICANT: Reinders, J.

; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.

; TITLE OF INVENTION: Transgenic Plant and Methods

; FILE REFERENCE: sequence

; CURRENT APPLICATION NUMBER: US/09/538,414

; CURRENT FILING DATE: 2000-03-29

; NUMBER OF SEQ ID NOS: 11

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 6

; LENGTH: 451

; TYPE: PRT

; ORGANISM: Fusarium graminearum

US-09-538-414-6

Query Match 100.0%; Score 2334; DB 4; Length 451;
Best Local Similarity 100.0%; Pred. No. 5.5e-234;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	MAFKIQDLTGQLPGLLSIY	101	VPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV	60
Db	1	MAFKIQDLTGQLPGLLSIY	101	VPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQV	60
Qy	61	KARGEISGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIAPRK	120		
Db	61	KARGEISGNTGTSFIVPFEDVPRVVKDLRDDPSAPTEGMRKAGYPMAMFENIAPRK	120		
Qy	121	TLPIGCTGDDPKPVILLQLNFKGLILTVNGQHGMDMVGQDAVIRLLSKACRNDPF	180		
Db	121	TLPIGCTGDDPKPVILLQLNFKGLILTVNGQHGMDMVGQDAVIRLLSKACRNDPF	180		
Qy	181	TEEMTAMNLDRTKIIVPYLENYTIIGPEVDHQIVKADVAGGDAVLTVPVSAWAFETSPKA	240		
Db	181	TEEMTAMNLDRTKIIVPYLENYTIIGPEVDHQIVKADVAGGDAVLTVPVSAWAFETSPKA	240		
Qy	241	MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAFTEFCRAVDARPMG	300		
Db	241	MSELKDAATKTLDASTKFKVSTDDALSAFIWKSASRVRLERIDGSAFTEFCRAVDARPMG	300		
Qy	301	VSNYPGLLONMYHNSHTTGEITANESIGATASRLSELDPASMRQTRGLATYHNNPDK	360		

Db 301 VSNVYGLLQNNYTHNSTIGETIANESLGATASRLRSELDPASMRQTRGLATYLNHNPK 360
QY 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRRPIPEPVESLWYFMPKPD 420
Db 361 SNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRRPIPEPVESLWYFMPKPD 420
QY 421 GFCAALSURDEDMRLKADKWKYQYVG 451
Db 421 GFCAALSURDEDMRLKADKWKYQYVG 451

RESULT 2

US-09-538-414-2
; Sequence 2, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Fusarium sporotrichioides
US-09-538-414-2

Query Match 79.7%; Score 1860.5; DB 4; Length 459;
Best Local Similarity 77.6%; Pred. No. 1e-184;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
QY 2 AFKIDTLGQLGLLSIYQISLLYVPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVK 61
Db 11 SFDIEDIIQQPPLLSIYQISLLYVPVSDSSQYPTIVSTFEQGLKRLSQTFFPWVAGQVK 70
QY 62 AEGISGNTGTSFIVPEFVPRVVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRKT 121
Db 71 TEGISGNTGTSKIIPEETPRIVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRKT 130
QY 122 LPICPGTGPDDPKPVILLQLNFIKGGILLTVNGQHGAMDMVGQDAVIRLLSKACRNDPFT 181
Db 131 LAIGPGNGPNDPKPVILLQLNFIKGGILLTVNGQHGAMDMVGQDAVIRLLSKACRNSFT 190
QY 182 EEMTAMNLDRTKIVPYLENYTIGPEVDHQAIVKADVAGGDAVLTVPVSAWAFPTFSKAM 241
Db 191 EEBISAMNLDRTKIVPYLENYTIGPEVDHQAIVKADVAGGDAVLTVPVSAWAFPTFSKAL 249
QY 242 SELKDAATKTLDASTKFEVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPA 301
Db 250 SELKDAATKTLDASTKFEVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPA 309
QY 302 SNVYGLLQNNYTHNSTIGETIANESLGATASRLRSELDPASMRQTRGLATYLNHNPKS 361
Db 310 SSVYGLLQNNYTHNSTIGETIANESLGATASRLRSELDPASMRQTRGLATYLNHNPKS 369
QY 362 NVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRRPIPEPVESLWYFMPKPD 421
Db 370 SVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRRPIPEPVESLWYFMPKPD 429
QY 422 EFCAALSURDEDMRLKADKWKYQYVG 451
Db 430 EFTASISURDEDMRLKADKWKYQYVG 459

RESULT 3

US-09-538-414-8
; Sequence 8, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patent In Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-09-538-414-8
Query Match 41.2%; Score 962.5; DB 4; Length 474;
Best Local Similarity 44.4%; Pred. No. 2.9e-91;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;
QY 6 QLDITGLQGLLSIYQISLLYVPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 65
Db 22 QLDITGLQGLLSIYQISLLYVPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 81
QY 66 SEGNTGTSFIVPEFVPRVVVKDLRDDPSAPTTIEGMRKAGYPMAMFENIIAPRKT-PI 124
Db 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMDSLEKADFPIYMLDEKTFAPCMTINPP 140
QY 125 GPOTG-PDDPKPVILLQLNFIKGGILLTVNGQHGAMDMVGQDAVIRLLSKACRNDPETER 183
Db 141 GNTIGMAAKSGPVFAVQANFISGGLVLTIVGQHNIMDITQESIIINLKNKSHQKPPSDE 200
QY 184 EMTAMNLDRTKIVPYLENYTIGPEVD-HQIVKA--DVAGDAVLTVPV--ASWAFPTFS 238
Db 201 ELIIGNIDKSKSILPDE-TWEPDTILVHEIVTSRNTSCEEKEQSCSSNSTWAYVFEFA 259
QY 239 KAMSELKDAATKTLDASTKFEVSTDDALSFAFWKSASRVRLERIDGSAPTEFCRAVDARPA 298
Db 260 ISLQNLRIILAMQCTSGTKFEVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVXR 319
QY 299 MGVSNNYVGLLQNNYTHNSTIGETIANESLGATASRLRSELDP--SMRQTRGLATYLN 356
Db 320 LGLPETYPGLLVNMTNTGSLKSLDHKSLGVLASQIRKRLDPKVDFDIAYNTCALATLSR 379
QY 357 NPKSVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPEVTRRRPIPEPVESLWYFMP 416
Db 380 CPDKTKVSIQPDITLSCGIVSWAKVGLWDYDFGLGKPEVTRRRPIPEPVESLWYFMP 439
QY 417 KPEDGEFCAALSURDEDMRLKADKWKYQYVG 451
Db 440 RSSRGEVMVALCLRDKDWECINADKENTVATHIG 474

RESULT 4

US-09-457-046B-56
; Sequence 56, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 56

```
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxis cuspidata
US-09-457-046B-56

Query Match      6.1%; Score 142; DB 3; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.9e-06;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;

Qy 5 IQLDTLGPGLLSITYTOISLLYPVSDSQYPTIVSTFEQGLRSEAVPVWAGQVKAEG 64
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
35 LQLSAVDRLPGMKFATFSAVLVYNASSHSIFANPAQIIHQALSKVLQYYPAGRIQKE 94
Qy :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
65 ISE-----GNIGTSPIVPEFVPRVVVKDLRDDPSAPITIEGRKAGYPMAMFENIIAPR 119
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
95 NEELEVECTGCGALFVEALVNDLSVLRLD-----DAQNASYEQLLF----- 136
Qy 120 KTLPIGPGTGPDDPKPVLILQLNFIKGLILITVNGHQGAMDMVGQDAVIRILSKACRND- 178
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
137 -SLP--PNIQVDLHPLILQVTRFTCGFVGVGVGFHHGICDARGTQFLOGLADWARGET 193
Qy 179 -PFTEEMTAMNLDKTIIV-----VLENTYTGPEVDHQIVKADVAGGDAVLTTPVSASWAF 233
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
194 KPLVEPVW-----NRELKIPEDLMHLOFHKEG--LIROPLKLD-----EICQAS 235
Qy 234 FTFSKAMSELKDAATKTLDASTKFTVSTDDALSAPIWKSASRVRLERIDGSAFTFCRAV 293
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
236 FTINSEIINYKQC---VIEECNEIFSAFEVVVALTW--IARTKAFQIPHENVMMLFGM 290
Qy 294 DARPAMGVSNYPGLLQNMTHNSTIG-----EIANESLGATASRLSELDPASMR 344
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
291 DARYEN-----PPLPKG--YIGNAIGTSCVIENVDLLNGSLSKAVMITKSKLIPIEN 343
Qy 345 QRTGLATYLNNDPKSNVSTADAPSTVMSLWAKVGLWDYDFGLG 393
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
344 LRSRIVA-----NQSGVD--EELKENVNVGFGDWRRLGPEHVEFDGSG 383

RESULT 5
US-09-457-046B-62
; Sequence 62, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-62

Query Match      6.1%; Score 141.5; DB 3; Length 436;
Best Local Similarity 22.2%; Pred. No. 6.4e-06;
Matches 74; Conservative 56; Mismatches 133; Indels 71; Gaps 14;

Qy 135 PVILLQLNFIK--GGILITVNGHQGAMDMVGQDAVIRILSKACRN-----DPFTE----- 182
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
135 PVILLIQANFFSCGGLVITICVSHKITDNTSLAMFIRGWAESSRGLGTLIPSTFASEVFP 194
Qy 183 ---EEMTAMNLDKTIIVPLENTYTGPEVDHQIVKADVAGGDAVLTTPVSASWAFTEFSPK 239
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
195 KPLDELSPKMDRK-----BEVEE-----MSCVTKKFPVFDAS 226
Qy 240 AMSELKDAATKTLDASTKFTVSTDDALSAPIWKSASRVRLERIDGSAFTFCRAVDARPA 299
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
227 KIKKLRAKASENL---VKNPFRVEAVTALFWRVCTKV--SRLSLTP-----RTSVLQLIV 277
Qy 300 GVSNNYPGLLQNMTHNSTIGEIANESLGATASRLSELDPASMRQRTGLATYLNNDP 359
```

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Db 278 NLRGKVDSCENTIGNMUSMLIKNEE--AAIERIQDVVDEI---RRAKBIFSLNCKEMS 332
; TYPE: PRT
; ORGANISM: Taxis cuspidata
US-08-207-904-2
; Sequence 2, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
; APPLICANT: Tuttle, AnnMarie
; APPLICANT: Crossland, Lyle D.
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,904
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,242
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: CGC 1624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919) 541-8615
; TELEFAX: (919) 541-8689
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-207-904-2

Query Match      5.7%; Score 134; DB 1; Length 448;
Best Local Similarity 21.7%; Pred. No. 4e-05;
Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;

Qy 21 TQISLLY-----PVSDSQYPTIVSTFEQGLR-----FSEAVPVWAGQVKAEG 64
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
34 THVTIYYIRFCHDCLEPSTDN---IITKRTSLSKALVHFYPLSGRLRWIAG-----S 83
Qy 65 ISENGTGTSTFVPEFVPRVVVKDLRDDPSAPITIEGRKAGYPMAMFENIIAPR--KTL 122
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
84 RLELDNCASGIVLMEATEAKLDLDGDFSPSP-----DLNLSFPRVDYTI 128
Qy 123 PIGPGTGPDDPKPVLILQL--NFIKGLILITVNGHQGAMDMVGQDAVIRILSKA--CRNDP 179
Db :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
129 PI-----DELPLLFVLTKFCQGGIALSFALSHAVVD--GQSALYFLETWASLARGE 179
Qy 180 FTEEMTAMNLDKTI-----VPYLENTYTGPEVDHQIVKADVAGGDAVLTTPVSASW 231
```

Db 180 LGNEPH-----DRKFRAGEPIAYTFEHLQNP-----PPLLGGSS- 220
QY 232 APFTFSPKAMSELKDAATKTLDASTKVF-----STDDALSAPIWKSASRVL 278
Db 221 -----EEEKNETKSGMLKLTQHVEMLRKKANQNGRSYTRYEVVTAHWRACKARG 275
QY 279 ERIDGSAPTFCRAVDARPA--GVSNYPGLLQNTYHNSITIGETANESLGATASRLS 336
Db 276 HKFE--OPTNLCICVNRIMQPLPKSYFGNAIVDIANGVSGDITSRPLEVAVRVR- 332
QY 337 ELDPASMRQTRGLAT-----YLHNPDKSNVSLTAD-----ADPSTSVMLSSW 380
Db 333 -----AAIKWTSYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPLGVI--SW 383
QY 381 AKVGLWDYDFGLGKPEVTRRIFEPVSLMYFMP-KKPDGFCAALSRLDEDMRLK 438
Db 384 ISPLLLGLDFGWG---KEIHMSPTHEYDGDGVILPCKEGDGLTVAAILQAVHVDFAK 439

RESULT 7

US-08-207-904-17
; Sequence 17, Application US/08207904
; Patent No. 5477002
; GENERAL INFORMATION:
; APPLICANT: Tuttle, AnnMarie
; APPLICANT: Crossland, Lytle D.
; TITLE OF INVENTION: Anther-Specific cDNA Sequences, Genomic
; TITLE OF INVENTION: DNA Sequences and Recombinant DNA Sequences
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CIBA-GEIGY Corporation
; STREET: 7 Skyline Drive
; CITY: Hawthorne
; STATE: New York
; COUNTRY: USA
; ZIP: 10532
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/207,904
; FILING DATE:
; CLASSIFICATION: 800
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/07/908,242
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Lazar, Steven R.
; REGISTRATION NUMBER: 32,618
; REFERENCE/DOCKET NUMBER: CGC 1624
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (919)541-8615
; TELEFAX: (919)541-8689
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 448 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-207-904-17

Query Match 5.7%; Score 134; DB 1; Length 448;
Best Local Similarity 21.7%; Pred. No. 4e-05;
Matches 104; Conservative 58; Mismatches 183; Indels 134; Gaps 24;
QY 21 TQISLLY-----PVSDSSQYPTIVSTFEQGLK-----FSEAVPWVAGQVKAEG 64
Db 34 THVPTIYRFFCHDCLPSTDN-----IKTURTSLSKALVHFYPLSGRLRWIAG-----S 83
QY 65 ISEGNIGTSFTVPPEDVRVVKLDLDDPSAPTEGMRKAGYPMAMFDENIAPR--KTL 122

Db 84 RLELDCNAGSIVLMEAFTEAKLDDLDGDFSPS-----DLNSLFPDYDTI 128
QY 123 PIGPGTGPPDPKREVILLQL-NFIKGLIILTVNGQHGAMDMVGQDAVIRLLSKA--CRNDP 179
Db 129 PI-----DELPLIFVQLTKFQCGGIALSFALSHAVVD--GOSALYFTLWASLARGEP 179
QY 180 FTEEMETAMNLDKTI-----VPYENYITIGPEVDHQIVKADVAGGDAVITPVSAW 231
Db 180 LGNEPH-----DRKFRAGEPIAYTFEHLQNP-----PPLLGGSS- 220
QY 232 APFTFSPKAMSELKDAATKTLDASTKVF-----STDDALSAPIWKSASRVL 278
Db 221 -----EEEKNETKSGMLKLTQHVEMLRKKANQNGRSYTRYEVVTAHWRACKARG 275
QY 279 ERIDGSAPTFCRAVDARPA--GVSNYPGLLQNTYHNSITIGETANESLGATASRLS 336
Db 276 HKFE--OPTNLCICVNRIMQPLPKSYFGNAIVDIANGVSGDITSRPLEVAVRVR- 332
QY 337 ELDPASMRQTRGLAT-----YLHNPDKSNVSLTAD-----ADPSTSVMLSSW 380
Db 333 -----AAIKWTSYANSTIDFLKNQEDLSKYQ---DIHAFRSKEGPFYGNPLGVI--SW 383
QY 381 AKVGLWDYDFGLGKPEVTRRIFEPVSLMYFMP-KKPDGFCAALSRLDEDMRLK 438
Db 384 ISPLLLGLDFGWG---KEIHMSPTHEYDGDGVILPCKEGDGLTVAAILQAVHVDFAK 439

RESULT 8

US-09-457-046B-28
; Sequence 28, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-28

Query Match 5.7%; Score 132; DB 3; Length 439;
Best Local Similarity 20.0%; Pred. No. 6.3e-05;
Matches 90; Conservative 78; Mismatches 183; Indels 98; Gaps 21;

QY 5 IQDLTLGQLPGLLSIYTOISLLYPVSDSSQYPTIVST-----PEQGLKRFSEAVPWVAGQ 59
Db 27 LQLSSIDNLPVGRGSIFNALLIYNAPS---PTMISADPAKPIREALAKILVYPPFAGR 83
QY 60 VK-----AEGISEGNTGTSFTIVPPEDVRVVKLDLDDPSAPTEGMRKAGYPMAMF 111
Db 84 LRETENGDLVECTGE---GAMFLEAMADNELSVLGDG---DDSNPSPQOL-----LF 130
QY 112 DENIIAPRKTLPIGPGTGPPDPKREVILLQLNFIKGLIILTVNGQHGAMDMVGQDAVIRLL 171
Db 131 -----SLPL--DTNFKDLSLLVVQVTRFTCGGFVGVSVFHHGVCDDGRGAQFLLKGL 179
QY 172 SKACRN-----DPFTEEMETAMNLDKTIVPYENYITIGPEVDHQIVKADVAGGDAVLT 225
Db 180 AEMARGEVKLSLEPIWNRRELVKLD-DPKYLQFFHFEFLRAPSIVEKIVQ----- 227
QY 226 PVSASNAFFTSPKAMSELKDAATKTLDASTKFTVSTDDALSAPTKWKSASRVLRIIDGSA 285
Db 228 -----TVFIIDFTETINVIKQS-----VMEECKEFCFSFEVASAMTW--IARTAFQIPESE 276
QY 286 PTEFCRAVDARPA--GVSNYPGLLQNTYHNS--TIGETANESLGATASRLS---ELD 339
Db 277 YVKILFGDMR-----NSFNPLPSGYGNSIGTACAVDINVQDLSGLLRALMIKKK 330

```
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 69
; LENGTH: 451
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-69

Query Match      5.6%; Score 130.5; DB 3; Length 451;
Best Local Similarity 21.7%; Pred. No. 9.4e-05;
Matches 105; Conservative 64; Mismatches 195; Indels 119; Gaps 25;

QY 8 DTLGQLPGLLSIYQISLLYPVSDSSQVPTIVSTFEQGLKRFSEAVPWAGQV----- 61
Db 29 DQVGTITHTIPTL-----FYDKPSESFGQNVVEILKTSLSRVLVHFVPMAGRLWLPGR 83
QY 62 -----AEGI-----SENGTGTSTFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMA 109
Db 84 FELNCNAGVEFIEARESGK-----LSDFKDFSTPEFENL----- 119
QY 110 MFDENIITAPKTLPIGPGTGPDDPKPVILLQLNFI--GGLILTVNGQHGAMDMVGQDAVI 168
Db 120 MPQVYNKPIETIPL-----FLAQVTFKCGGISLVNVSIAVD--GQSA-L 164
QY 169 RLLS--KACNDPTEEMTAMNLDRTI--VPYLENYTIGPEVDHQ----- 211
Db 165 HLISEWGRGLARGEPL-----TVPELDRKILWAGER-LPPFVSPPKFDHKEFDQPPFLIGE 219
QY 212 --IVKADVAGDAVLTVPVSASWAFETSPKAMSELKDA--TKILDASTKFSVTDALSA 267
Db 220 TDNVEERKKKTIIVNMLPLSTS-----OLQKLRSKANGSKHSDPAKGP-TRYETVIG 269
QY 268 FIKWSASRVLERIDGSAPTEFCRAVDARPAM--GVSNYPGLLQNMVYHNSTIGEIANE 325
Db 270 HVWRACKACKARGH--SPQPTALGICIDTRSRMEPPLRGYFGNATLDVVAASTSGELISN 327
QY 326 SLGATASRLSELDPASMRQTRGLATYLNHNPDKSNVSLTA-----DADPSTSV 376
Db 328 ELGFAASLISKAIKNVTNEYVMIGI-EYLKNQDKLKKFQDLHALGSTEGPPYGNPLGVV 386
QY 377 LSSWAKVGLWDYDGLGKGPETVRRPIFEVESLMYFMP-KKPDGFECAALSDEDM 435
Db 387 --SWITPMYGLDFGWG---KEFTYGTGTHDFDGSILPLQDNEDSGSVILATCLQVAHME 441
QY 436 RLK 438
Db 442 AFK 444

RESULT 10
US-09-457-046B-60
; Sequence 60, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 69
; LENGTH: 451
; TYPE: PR1
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-60

Query Match      5.4%; Score 126.5; DB 3; Length 435;
Best Local Similarity 20.2%; Pred. No. 0.00023;
Matches 99; Conservative 77; Mismatches 182; Indels 133; Gaps 26;

QY 4 KIQLDTLG-QLPGLLSIYQISLLYP-VSDSSQVPTIVSTFEQGLK-----RFSEAVPW 56
Db 23 RLQLSILDLYCPG---IYVSTIFFYDLITSESE-----VFSENKLKLSLSETLSRFYP-L 72
QY 57 AGOVKAEGISGNGTGSTFIVPFEDVPRVVVKDLRDDPSAPTIEGMRKAGYPMAFENII 116
Db 73 AGRIEGLISCNDEGAVTEARTD---LILLPDFLRNLNMTDLSLGP----- 114
QY 117 APRKTLPI-IGPGTGPDDPKPVILLQLNFI--KGGILITVNGQHGAMDMVGQDAVIRLLSK 173
Db 115 -----LPTLAAGESP-AAWPLLSVKVTFFGSGSGVAVSVSHKICDIASLTVFK----- 164
QY 174 ACRNDPTEEMTAMNLDRTIIVYLENYTIGPEVDHQIVKADVAGDAVLTVPVSASWAF 233
Db 165 ----DWAT---TTAKGKSNSTI-EFAETTYIPPPSHMYEQFPSTDSNIT---SKYVL 213
QY 234 --FTFSPKAMSELK-DAATKTLDASTKFSVTDALSAFIKSA----- 273
Db 214 KRFFVEFSKIAELKHKAASESVPVPTRV---EAIMSLIMRCARNSRSSNLLIPROAVMW 269
QY 274 -----SRVLERIDGSAPTEFCRAVDARPAMGVSNYPGLLQNMVYHNSTIGEIA 323
Db 270 QAMDIRLIRIPSSVAPKDVIGNLQSGFSLKKDAESEFEI---PEIVATFRKNKERVNEMI 325
QY 324 NESIGATASRLSELDPASMRQTRGLATYLNHNPDKSNVSLTA--ADPSTSV---MLSS 379
Db 326 KESLQG-----NTIGQSLLSLMAETVSESTEIDRYIMSS 359
QY 380 WAKVGLWDYDGLGKGPETV---RRPIFEVESLMYFMPKKPDGFECAALSDEDM 436
Db 360 WCRKPFYEVDF--GSGSPVWVGYSHTIYDNMVGVLIDSKEGDG-VFAMISLPEEDMSV 416
QY 437 LKADKEWTKYA 447
Db 417 FVDDQELLAYA 427

RESULT 11
US-09-457-046B-68
; Sequence 68, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croceau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent in Ver. 2.1
; SEQ ID NO 68
; LENGTH: 439
; TYPE: PR1
; ORGANISM: Catharanthus roseus
US-09-457-046B-68
```

Query Match 5.4%; Score 125.5; DB 3; Length 439;
Best Local Similarity 20.5%; Pred. No. 0.0003;
Matches 95; Conservative 75; Mismatches 193; Indels 101; Gaps 23;

QY 18 SIY---TQISLAYPVSDSSQYPTVTFBQGL-KRFSEAVPVWVAGQVKAEGISEGNTGTS 73
DB 39 NIYQTCVSVGFYENPDGIEISTIREQLQNSLTKTLVSVYPFAGKVKNKYIHCNDGDGIE 98
QY 74 FIVPFEDVRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPKTLPIGPGTGPDP 133
DB 99 FV---EVRIRCRMNDI-----LKYELSYARDLVLPKRV-----VGSDET 136
QY 134 KPVIILQMLFIKGLILTVNGQHGAMDMVQDQDAVIRLLSK-----ACRNDPFTTEEWMTAM 188
DB 137 TAIVQLS-HFDCGLAVAGISH-----KVADGGTIFASFMKOWAASAC-----YL 180
QY 189 NLRDKTIVPLENTYTGPEVDHQIVKADVAGDAVITPVASWA---FFTFSPKAMSELKD 246
DB 181 SSSHVPTPLLVGDSIFPRQDNIICEQ-----FPTSNCVKEKTFIPPPPEAIEKIK- 230
QY 247 AATKTLDAKTFVSTDDALSAPTIKSA-----SRVLERIDGSAPTEFCRAVDARPAWGV 301
DB 231 --SKAVEFGIEKPTRVETVLTAFLSRCATVAGKSAKNNNGQSLPFPVLQAINLRPILLE 288
QY 302 SNNYPCGLQNMTHNSTIGETIANESLG-----ATASRLRSELDPSMRQRTGLA----- 351
DB 289 PQNSVGNLVSII-YFSRTIKE--NDYLNKEYTKLVINELRKE-----KQIKNLREKL 339
QY 352 TYLHNNPD-----KSNVSLTADAPSTSVMLSSWAKVGLWMDYDFGLGKGPRTVRRPIF 405
DB 340 TYVAQMEEFVKSLEKFEIDISNFLDID---AVLSDSWCRPFYDVF--GWGKPIWV--CLF 392
QY 406 EPVESLMYFMPKPDGE---FCAALSRLRDEMDRLKADKEWKY 446
DB 393 QPYIKNCVMMDPYFGDDYDYGIAIVSFEQEKMSAFEKNEQLQF 436

RESULT 12
US-09-457-046B-73
; Sequence 73, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 73
; LENGTH: 445
; TYPE: PRF
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-73

Query Match 5.3%; Score 124; DB 3; Length 445;
Best Local Similarity 19.6%; Pred. No. 0.00044;
Matches 99; Conservative 79; Mismatches 176; Indels 126; Gaps 23;

QY 20 YTOISLILPVSDSSQ---YPTIVSTFBQGL-KRFSEAVPVW---VAGQVKAEG-----ISE 67
DB 37 HTGAVLIYKQPDNEDNIHPSSSMYFDANILIEALSALVPFYPMAGELKINGDRYBIDC 96
QY 68 GNTGTSTIVPEFDPVRVVKDLRDDPSAPTEGMRKAGYPMAMFENIIAPKTLPIGPG 127
DB 97 NAEALPV---EASSHVLEDFGD--FRPNDE-LHRVMVPTCDYSKGI----- 138
QY 128 TGPDDPKPVILLQI-NFTKGLILTVNGQHGAMDMVG-----QDAV 167
DB 139 -----SSPFLMVQLTRFCGVSTIGFAGHHVCDGMHAFBNNSWARIKGLLPALFVH 194
QY 168 IRLSKACRNDPFTTEEWMTAMNLRKTIIVPLENTYTGPEVDHQIVKADVAGDAVITPV 227

DB 195 DRYLHLRPNRP---QIKYSHSQFEPFVPSLPNELLDGK-----T 231
QY 228 SASWAFTEFSPKAMSELKDAATKTLDAS--TKFVSTDDALSAPFIKWSASRVRLERIDGSA 285
DB 232 NKSQTLFILSRQINILK---QKLDLSNNTTFLSTYEVVAHVWRSVKAR--GLSDHE 285
QY 286 PTEFCRAVDARPAW---GVSNNYPGLLQNMTHNSTIGETIANESLGATASR----- 333
DB 286 EIKLIMPVDGRSRINNPSPKGYCGNVFLAVCTATVGDLSCNPLTDTAGKVQEAALKGLD 345
QY 334 ---LRSELDPASMRQRTGLATVHLNPNKSNVSLTADADPSTSVMLSSWAKVGLWMDYDF 390
DB 346 DDIYLRSAIDHTESKP---GLPVEYMGSPKTLV-----PNVLVNSMGRIPYQAMDF 393
QY 391 GLGLGKGPETVRRPIEPFVESLAMY-----FMPKKEP-DGEFCAALSRLRDEMDRLK 438
DB 394 GWG-----SPTFFGIGNIFDGGCFLIPSRDGGSGMTLAINLFPSSHLRSEK 439

RESULT 13
US-09-457-046B-66
; Sequence 66, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 66
; LENGTH: 433
; TYPE: PRF
; ORGANISM: Clarkia breweri
US-09-457-046B-66

Query Match 5.2%; Score 122; DB 3; Length 433;
Best Local Similarity 20.3%; Pred. No. 0.00067;
Matches 97; Conservative 64; Mismatches 196; Indels 122; Gaps 19;

QY 17 LSIYTOISLILPVSDSSQYPTI-----VSTFQGLKRFSEAVPVWVAGQVKAEGISEG 69
DB 26 LSLDQIQIPFYVGLIFHYETLSDNSDITLSKLESSLSETLTLYHYHAGY----- 76
QY 70 TGTSTIVPEFDPVRVVKDLRDDPSAPTEGMRKAGYPMAMFENI---IAPRKT 122
DB 77 NGTDCVIECND-----QGI---GIVETAFDVELHQLGELLESNNL 115
QY 123 PIGFG--TGPDDPKPVILLQILNFIK--GGLILTVNGQHGAMDMVQDQDAVIRLLSKACRNDP 179
DB 116 LVGLSGFLSETETPPLAAIQLNMFKCGLVIGAQFNHILIGDMFTMTSMNSWAKACR-- 172
QY 180 FTEEMTAMNLRKTIIVPLENTYTGPEVDHQIVKADVAGDAVITPVASWAFTEFSPK 239
DB 173 VGIKEVAHPTFGLAPLMPSAKVLNIPPPSPFEGVKF-----VSKR---FVFEN 218
QY 240 AMSELKDAATK-----TLDASTKFSVSTDDALSAPFIK----- 272
DB 219 AITRLRKEATEEDGGDDDDOKKRPSRVDLIVTAFPLSKSLIEMDCAKKEQTKSRPSLVMH 278
QY 273 ---ASRVRLERIDGSAPTEFCRAVDARPAWGVSNPNYEGLLQNMTHNSTIGETIANESLGA 329
DB 279 MNLKRKTKL-ALENDVSGNFFIVVNAESKITVAPKITDLETSL---GSAOCEIISRVAKV 334
QY 330 TASRLRSELDPSMRQRTGLATVHLNPNKSNVSLTADADPSTSVMLSSWAKVGLWMDYD 389
DB 335 DDAFVSSVMLNSVRE-----FYEWKGEKNVFL-----YTSRCRPLFEVD 377
QY 390 FGLGL-GKPEVTRRPIEPVESLMYFMPKPDGEFCAALS-LRDEMDRLKADKEWKY 446
DB 378 FGWGPISLVDITAVPF-----GLIVLMDAPAGIACVACLSLSEHMIQOHHQLLSY 431

RESULT 14

US-09-457-046B-22
; Sequence 22, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 22
; LENGTH: 306
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-457-046B-22

Query Match 5.2%; Score 121.5; DB 3; Length 306;
Best Local Similarity 20.7%; Pred. No. 0.00042;
Matches 59; Conservative 44; Mismatches 113; Indels 69; Gaps 10;
QY 135 PVILLQLNFIKGGILITVNGOHGMDVMVQDAVIRLLSKACRNDPTEBEETAMNLDKRT 194
DB 64 PLLAVQATKLDGIALAVTNHAVADATSVWHFISSWAQLCK-----EPS 108
QY 195 IVPYLENY-----TTGPEVDHQIVKADVAGDAV-----LTPVSASWAFFTFSPKAMSE 243
DB 109 NIPLPLHTRCFTTISP-----IKLDIQSSTTTESIDNFPPLTEKIHFSKTIISR 162
QY 244 LKDAATKTLDASTREKSTDDALSARIKWSASRVRLERIDGSAPTFCRAVDARPAAM--GV 301
DB 163 LKEAMEACKSKSISISSFQALCGHLWQSITRAR--GLSPSEPTTIKIAVNCRPIVPEPL 220
QY 302 SNYPGLLQNNMTYHNSTIGEIANESLGATA-----SRLSELDPASMRQTR 348
DB 221 PNVYFGNAVQVVDVTMTTEILLGNG-GACAAILLHQKISAHQDTQIRAEILD----- 270
QY 349 GLATYLNHNNPKSNVSLTADAPSTSVMLSSWAKVGLWDYDFGLG 393
DB 271 -----KPKK--IVHTNNLIPCNIIAMAGSPRPPIYNNDFGWG 305

RESULT 15

US-09-457-046B-63
; Sequence 63, Application US/09457046B
; Patent No. 6287835
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/457,046B
; CURRENT FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 63
; LENGTH: 482
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-457-046B-63

Query Match 5.2%; Score 121.5; DB 3; Length 482;
Best Local Similarity 19.5%; Pred. No. 0.00091;
Matches 99; Conservative 76; Mismatches 204; Indels 129; Gaps 21;
QY 9 TLGOLPGLSLIYTOISLLYPVSDSQYPTIVYSTFEQGLKRFSEAVPWAGQVKAEG----- 64
DB 30 SVSLLPMLSCHYIKGCLUF--TCPNLPALPLSHLKHLSISITLTHFFPLAGRLSTSSSGHV 88
QY 65 -ISEGNTGTSTF-----IVPFEDVRVVVKOLRDDPSAPTIEGMRKAGYPMAMF 111
DB 89 FLTCDNAGADVFQAQAKSIHVSVDVIAGIDVPD--VVKPEFTYDRAVSIEGHN----- 138

QY 112 DENIIAPRKTLPIGGTGDDPKPVILLQLNFIKGGILITVNGOHGMDVMVQDAVIRLL 171
DB 139 -----RPI LAVQVTEINDGVFIGGSVNHAVTDGTSLNWFI----- 173
QY 172 SKACRNDPTEBEETAMNLDKRTIVPYLENYTTIGPEVDHQIVKADVAGDAVLTVPVSASW 231
DB 174 -----NTFAEVSRGAKNVTQPDFT-RESVLISPAV-----LKVP-QGGPKVTFDENAPL 221
QY 232 --AFTFSFKAMSELKDAATKTL----- 252
DB 222 RERIFSPRESIQELKAVVNKKKWLTVNGEIDGVVELLGKQSNCKLNGKENGILTEMLFS 281
QY 253 -----DASTKVFSTD-----DALSARIKWSASRVRLERIDGSAPTFCRAVDARPAWGSN 303
DB 282 LFGRNDAYSKPVAVEISSFQSLCALLWRAITRAR--KLPSSKTTTTFRMAVNCRHLSPKL 339
QY 304 N---YPGLLQNM-TVHNSTIGEIANESLGATASRLRSELDPASMRQTRGLATYLHNNDP 359
DB 340 NPEYFGNAIQSVPTP--ATAAEVLSRDLKWCADQLNQSV-AAHQDGRIRSVVADWEANP- 395
QY 360 KSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKPKETVRRPIFEFVESIMYMP-KK 418
DB 396 --RCFPLGNAD-GASVTMGSSSPRPMPYDNDP--GWRPVAVRSGRSNKFDGKISAFPGRE 450
QY 419 PDGEFCAALSRLDEDMRLKADKWKTKY 446
DB 451 GNGTVDLEVVLSPETMAGIESDGEFMR 478

Search completed: February 7, 2004, 23:48:38
Job time : 73 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: February 7, 2004, 23:46:34 ; Search time 249 Seconds
(without alignments)
379.243 Million cell updates/sec

Title: US-10-614-954-6

Perfect score: 2334

Sequence: 1 MAFKIQDITGLQGLLSIY.....EDMDLXADKRWTKYAQVVG 451

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 801455 seqs, 209382283 residues

Total number of hits satisfying chosen parameters: 801455

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/1/pubpaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/1/pubpaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/1/pubpaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/1/pubpaa/US09C_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/1/pubpaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Length	DB	ID	Description
1	2334	100.0	451	14	US-10-074-279-6	Sequence 6, Appli
2	1860.5	79.7	459	14	US-10-074-279-2	Sequence 2, Appli
3	962.5	41.2	474	14	US-10-074-279-8	Sequence 8, Appli
4	170.5	7.3	436	14	US-10-078-929-64	Sequence 64, Appl
5	168.5	7.2	446	14	US-10-078-929-52	Sequence 52, Appl
6	161	6.9	439	14	US-10-078-929-60	Sequence 60, Appl
7	144	6.2	431	14	US-10-078-929-200	Sequence 200, App
8	142	6.1	448	10	US-09-866-572A-56	Sequence 56, Appl
9	142	6.1	448	10	US-09-866-570A-69	Sequence 56, Appl
10	142	6.1	448	12	US-10-166-984-56	Sequence 56, Appl
11	142	6.1	448	15	US-10-166-984-56	Sequence 56, Appl
12	141.5	6.1	436	10	US-09-866-572A-62	Sequence 62, Appl
13	141.5	6.1	436	10	US-09-866-570A-62	Sequence 62, Appl
14	141.5	6.1	436	12	US-10-166-984-62	Sequence 62, Appl
15	141.5	6.1	436	15	US-10-166-984-62	Sequence 62, Appl

16	132	5.7	439	10	US-09-866-572A-28	Sequence 28, Appl
17	132	5.7	439	10	US-09-866-570A-28	Sequence 28, Appl
18	132	5.7	439	12	US-10-166-984-28	Sequence 28, Appl
19	132	5.7	439	15	US-10-166-984-28	Sequence 28, Appl
20	130.5	5.6	451	10	US-09-866-572A-69	Sequence 69, Appl
21	130.5	5.6	451	10	US-09-866-570A-69	Sequence 69, Appl
22	130.5	5.6	451	12	US-10-166-984-69	Sequence 69, Appl
23	130.5	5.6	451	15	US-10-166-984-69	Sequence 69, Appl
24	126.5	5.4	435	10	US-09-866-572A-60	Sequence 60, Appl
25	126.5	5.4	435	10	US-09-866-570A-60	Sequence 60, Appl
26	126.5	5.4	435	12	US-10-166-984-75	Sequence 75, Appl
27	126.5	5.4	435	15	US-10-166-984-75	Sequence 75, Appl
28	125.5	5.4	439	10	US-09-866-572A-68	Sequence 68, Appl
29	125.5	5.4	439	10	US-09-866-570A-68	Sequence 68, Appl
30	125.5	5.4	439	12	US-10-166-984-68	Sequence 68, Appl
31	125.5	5.4	439	15	US-10-166-984-68	Sequence 68, Appl
32	124	5.3	445	10	US-09-866-572A-73	Sequence 73, Appl
33	124	5.3	445	10	US-09-866-570A-73	Sequence 73, Appl
34	124	5.3	445	12	US-10-166-984-73	Sequence 73, Appl
35	124	5.3	445	15	US-10-166-984-73	Sequence 73, Appl
36	122	5.2	433	10	US-09-866-572A-66	Sequence 66, Appl
37	122	5.2	433	10	US-09-866-570A-66	Sequence 66, Appl
38	122	5.2	433	12	US-10-166-984-66	Sequence 66, Appl
39	122	5.2	433	15	US-10-166-984-66	Sequence 66, Appl
40	121.5	5.2	306	10	US-09-866-572A-22	Sequence 22, Appl
41	121.5	5.2	306	10	US-09-866-570A-22	Sequence 22, Appl
42	121.5	5.2	306	12	US-10-166-984-22	Sequence 22, Appl
43	121.5	5.2	306	15	US-10-166-984-22	Sequence 22, Appl
44	121.5	5.2	482	10	US-09-866-572A-63	Sequence 63, Appl
45	121.5	5.2	482	10	US-09-866-570A-63	Sequence 63, Appl

ALIGNMENTS

RESULT 1

US-10-074-279-6
; Sequence 6, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 6
; LENGTH: 451
; TYPE: PRT
; ORGANISM: Fusarium graminearum
US-10-074-279-6

Query Match 100.0%; Score 2334; DB 14; Length 451;

Best Local Similarity 100.0%; Pred. No. 3.7e-222;

Matches 451; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MAFKIQDITGLQGLLSIYQTSLIYPVSDSSQYPTIVSTFEQGLKRFSEAVPWAGQV 60

Db 1 MAFKIQDITGLQGLLSIYQTSLIYPVSDSSQYPTIVSTFEQGLKRFSEAVPWAGQV 60

QY 61 KARGISEGNTGTGFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPRK 120

Db 61 KARGISEGNTGTGFIVPFEDVPRVVKDLRDDPSAPTIEGMRKAGYPMAMFENIAPRK 120

QY 121 TLPIGPGTGPDPKPKVILLQLNFIKGGLLITVNGOHGMDVGVQDAVIRLLSKACRNDPF 180
DB 121 TLPIGPGTGPDPKPKVILLQLNFIKGGLLITVNGOHGMDVGVQDAVIRLLSKACRNDPF 180
QY 181 TEEETAMNLDKRTIVPVLENTYITIGPEVDHQIVKADVAGDVAITPVSAWAFFTFSPKA 240
DB 181 TEEETAMNLDKRTIVPVLENTYITIGPEVDHQIVKADVAGDVAITPVSAWAFFTFSPKA 240
QY 241 MSELKDAATKTLDASTKFTVSTDDALSATFWKASRVRLERIDGSAFTFCRAVDARPAMG 300
DB 241 MSELKDAATKTLDASTKFTVSTDDALSATFWKASRVRLERIDGSAFTFCRAVDARPAMG 300
QY 301 VSNVYPLLQNTYHNTSTIGETANESLGATASRLSELDPASMBRQTRGLATVYLNHPDK 360
DB 301 VSNVYPLLQNTYHNTSTIGETANESLGATASRLSELDPASMBRQTRGLATVYLNHPDK 360
QY 361 SNVSLTADADPSTVSMSSWAKVGLWDYDFGLGKPEVTRRRPIFFPVESLMYFMPKPKD 420
DB 361 SNVSLTADADPSTVSMSSWAKVGLWDYDFGLGKPEVTRRRPIFFPVESLMYFMPKPKD 420
QY 421 GBFCAALSRLDEDMRLKADKWKYQAYVG 451
DB 421 GBFCAALSRLDEDMRLKADKWKYQAYVG 451

RESULT 2

US-10-074-279-2
; Sequence 2, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 2
; LENGTH: 459
; TYPE: PRT
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-2

Query Match 79.7%; Score 1860.5; DB 14; Length 459;
Best Local Similarity 77.6%; Pred. No. 3e-175;
Matches 349; Conservative 50; Mismatches 50; Indels 1; Gaps 1;
QY 2 AFKQIDTLQGLLSIYQISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVK 61
DB 11 SFDELDLIGQQPLLSIYQISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVK 70
QY 62 ARGISEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTTEGMRKAGYPMAMFENIIAPRKT 121
DB 71 TEGISEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTTEGMRKAGYPMAMFENIIAPRKT 130
QY 122 LPFGTGPDPKPKVILLQLNFIKGGLLITVNGOHGMDVGVQDAVIRLLSKACRNDPFT 181
DB 131 LAIPGNGPNDPKPKVILLQLNFIKGGLLITVNGOHGMDVGVQDAVIRLLSKACRNDPFT 190
QY 182 EETAMNLDKRTIVPVLENTYITIGPEVDHQIVKADVAGDVAITPVSAWAFFTFSPKA 241
DB 191 EETAMNLDKRTIVPVLENTYITIGPEVDHQIVKADVAGDVAITPVSAWAFFTFSPKA 249
QY 242 SELKDAATKTLDASTKFTVSTDDALSATFWKASRVRLERIDGSAFTFCRAVDARPAMG 301

DB 250 SELKDAATKTLDASTKFTVSTDDALSATFWKASRVRLERIDGSAFTFCRAVDMRGPMGV 309
QY 302 SNNYPLLQNTYHNTSTIGETANESLGATASRLSELDPASMBRQTRGLATVYLNHPDKS 361
DB 310 STYPLLQNTYHNTSTIGETANESLGATASRLSELDPASMBRQTRGLATVYLNHPDKS 369
QY 362 NVSLTADADPSTVSMSSWAKVGLWDYDFGLGKPEVTRRRPIFFPVESLMYFMPKPKD 421
DB 370 SVSLTADANPSSIMSSWAKVGCWEYDFGLGKPEVTRRRPIFFPVESLMYFMPKPKD 429
QY 422 EFCALSLRDEDMRLKADKWKYQAYVG 451
DB 430 EFTASISLRDEDMRLKADKWKYQAYVG 459
RESULT 3
US-10-074-279-8
; Sequence 8, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 8
; LENGTH: 474
; TYPE: PRT
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-8

Query Match 41.2%; Score 962.5; DB 14; Length 474;
Best Local Similarity 44.4%; Pred. No. 2.9e-86;
Matches 202; Conservative 84; Mismatches 158; Indels 11; Gaps 8;
QY 6 QLDTLQGLLSIYQISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 65
DB 22 QLDLQGLLSIYQISLLYVPVSDSSOYPTIVSTFEQGLKRFSEAVPWVAGQVKAEGI 81
QY 66 SEGNTGTSFTIVPPEDVPRVVVKDLRDDPSAPTTEGMRKAGYPMAMFENIIAPRKT-L-PI 124
DB 82 DEGNTGTYRIVPSDKIP-LIVQDLREDLSAPTMSLEKADFFIYMLDEKTFAPCMTINPP 140
QY 125 GPQGTG-PDDPKPVILLQLNFIKGGLLITVNGOHGMDVGVQDAVIRLLSKACRNDPTEE 183
DB 141 GNTIGMAAKSGPVFAQANFISGGLVLTIVGQINMDITQESLIINLNSCHKQPPSDE 200
QY 184 EMTAMNLDKRTIVPVLENTYITIGPEVD-HQIVKA--DVAGDVAITPVSAWAFFTFSP 238
DB 201 ELIGNIDKSKSLPDE-TWEPDTLVHVEIVTSRTSKEEKEQSCSSNTWAYVFESA 259
QY 239 KAMSELKDAATKTLDASTKFTVSTDDALSATFWKASRVRLERIDGSAFTFCRAVDARPA 298
DB 260 ISLQNLRLAMQCTSGTKFVSTDDIVTAFIWKSVSRARLSRLKPKETKSNLGRAVDVRKR 319
QY 299 MGVSNNYPLLQNTYHNTSTIGETANESLGATASRLSELDP--SMRQTRGLATVYLN 356
DB 320 LGLPETVPLLVNMTNTGSLSDHKSGLVLAQIRKLDPKVDFDLAYNTCALATLSR 379
QY 357 NPDKSNVSLTADADPSTVSMSSWAKVGLWDYDFGLGKPEVTRRRPIFFPVESLMYFMP 416
DB 380 CPDKTKVSIQPIQIDTLSGIWSWAKVSLVDVDFNLGLGKPEVTRRRPIFFPVESLMYFMP 439

Db 190 MPFIDRSLRLRDPPTPAYPHIEYQAPAPMLSEPPQAAALTSKPTPTTAVAFKLSRAEL 249
QY 242 SELKDAAYKTLDASTKFSVSTDDALSAFTWKSASRVRLERIDGSAPEFCRAVDAPAMGV 301
Db 250 VRLR-SQVPAREGAPRF-STYAVLAHVRCASLAR--GLPADQPTKLYCATDGRQL-- 303
QY 302 SNNYP---GLQNNYTHNSTTGEIANESLGAT--ASRLRSELDPASMRQRTGLATYLH 355
Db 304 ---QPLPEGYGNVIFTATPLANAGTVTAGVAGASVIAQAALDRMD-DGYCRSALDYLE 359
QY 356 NNPDKSNVSLTADADPSTSMVLSWAKVGLWDYDFGLGLGKPKETVRRPIPE-----PVES 410
Db 360 LQPDLSALVRGAHTFRCPNLGTSVWRLPIHDADFCWG-----RPVFMGPGGIAYREG 411
QY 411 LMYFMPK-KPDGEFCAALSIRDEMDRLK 438
Db 412 LAFVLPSANRDGSLSVASISLOAHEMEKFR 440

RESULT 6
US-10-078-929-60
; Sequence 60, Application US/10078929
; Publication No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Gao-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 60
; LENGTH: 439
; TYPE: PRT
; ORGANISM: Glycine max
US-10-078-929-60
Query Match 6.9%; Score 161; DB 14; Length 439;
Best Local Similarity 21.9%; Pred. No. 6.5e-07;
Matches 99; Conservative 72; Mismatches 195; Indels 86; Gaps 20;
QY 21 TQISLLYPVSDSSQYPIVTSFFEOGLKRFSEAVWAGVQVKAEGLSGNTGTSPFVFPED 80
Db 25 SNVDLVVVP---NFHTPSVYFTRPNSVNFDDA-----KWKKAISK-----VLVDFYP 69
QY 81 VPRVVVKDLRDDPSAPTI-----EGMR--KAGYPWAMFENIIAP-----RKTLPFGPGTGP 130

Db 70 ---MAARLRDDDDGRVEIYCDAGQVLFVEAETTAIEDFGDFSPTELEQLIPSVDSAG 126
QY 131 DDPKPVILLQANFIK-GGILLTVNGOHGAMDMVGQDAVIRLLSKACRNDPFTTEETAMN 189
Db 127 IHSYELLVLQVTFYKCGGVSIGVGMQHHVADGASGLHFINAWSDVAR-----G 174
QY 190 LDRKTIYPVLENYTIG-----PEVDHQIVKADVA-----GGDAVLTPVSAS 230
Db 175 LD-ISLPPIDRTLLRARPPPLPVFPHIEYKPPATKTTPLQPSKPLGSDSTAVAVST- 232
QY 231 WAPFTFSPKAMELKDAAKTKLDASTKFSVSTDDALSAFTWKSASRVRLERIDGSAPEFC 290
Db 233 ---FKLTRQDLSTLKGKSE--DGNITISYSSEMLAGHVWRSVCKAR--ALPDDQTKLY 285
QY 291 RAVDARPA--GVSNYPGLQNNYTHNSTTGEIANESLGATASRLRSELDPASMRQRT 348
Db 286 IATDGRARLQPPPLPHGYFNGVITTRIAVAGDLMSKPTWYAAASRPHDALIRMD-NEYLR 344
QY 349 GLATVILHNNPKSNVSLTADADPSTSMVLSWAKVGLWDYDFGLGLGKPKETVRRPIPE-- 406
Db 345 SALDYLELQPDLSALVRGAHTFRCPNLGITSWRLPIHDADFCWG-----RPIFMGP 396
QY 407 ---PVESLMYFMPKPKP-DGEFCAALSIRDEMD 434
Db 397 GGIAYEGLSFIIPSTNDGSLSLAIALRPEQM 428

RESULT 7
US-10-078-929-200
; Sequence 200, Application US/10078929
; Publication No. US20020152497A1
; GENERAL INFORMATION:
; APPLICANT: Rafalski, Antoni
; APPLICANT: Miao, Gao-Hua
; APPLICANT: Falco, Saverio Carl
; APPLICANT: Sakai, Hajime
; APPLICANT: Famodu, Omolayo O.
; APPLICANT: Odell, Joan T.
; APPLICANT: Meyers, Blake
; APPLICANT: Thorpe, Catherine
; APPLICANT: Weng, Zude
; TITLE OF INVENTION: Nucleic Acid Fragments Encoding Proteins Involved in
; FILE REFERENCE: BB1357 US NA
; CURRENT APPLICATION NUMBER: US/10/078,929
; CURRENT FILING DATE: 2002-02-19
; PRIOR APPLICATION NUMBER: 09/566,394
; PRIOR FILING DATE: 2000-05-05
; PRIOR APPLICATION NUMBER: 60/133038
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133042
; PRIOR FILING DATE: 1999-05-07
; PRIOR APPLICATION NUMBER: 60/133427
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133437
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133428
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133438
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/133436
; PRIOR FILING DATE: 1999-05-11
; PRIOR APPLICATION NUMBER: 60/137667
; PRIOR FILING DATE: 1999-06-04
; NUMBER OF SEQ ID NOS: 208
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 200
; LENGTH: 431
; TYPE: PRT
; ORGANISM: Ipomoea batatas
US-10-078-929-200

Query Match 6.2%; Score 144; DB 14; Length 431;
Best Local Similarity 24.68; Pred. No. 3e-05;
Matches 84; Conservative 48; Mismatches 153; Indels 56; Gaps 17;
QY 119 RKTLPICGTPGDDPKPVILLQLNFIK--GGILITVNGQHGAMDMVGQDAVIRLLSKACRN 177
DB 120 RKFTPTVDTSGDISFFLIIFQVTRFKGCVGLGTGVFHTLSDGVSSLIHINTWSDMARG 179
QY 178 -----DPTTEEMTAMNLDKRTIYPYLEN--YTTGPEVDHIOVKADVAGDAVLTPTVSAS 230
DB 180 LSAVPPFIDRTLLRA--RDPPTPAFHESEYDOPKLL--KSVPEKRGSS-----SAS 227
QY 231 WAFPTSPKAMSELKDAATKTLDASTKFSVDDALSAFIWKSASRVRLERIDGSAPTFC 290
DB 228 TTMLKITPEQLALK--TKSKHEG-----STYEILAHIIWCAKAR--GLTDDQATKLY 278
QY 291 RAVDAR-----PAMGVSNYPGLLQNMTHNSTI---GEIANESLGATASRLRSELDPASM 343
DB 279 VATDGRSLCPPLP-----PGYLGNNVVTATPMAESGELQSEPLTNSAKRIHSALSAMD- 332
QY 344 RQTRGLATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLGKDETVRPP 403
DB 333 DEYLRSALDFLECCPDLSKLIRGNSYFASPNLNINSWTRLPVHESDFGWG-----RP 384
QY 404 I-PEPV---ESLMYEMPK-KPDGEFCAALSRLDEDMRLK 438
DB 385 IHMGPAIIIEGTVIILPSPNKORTSLAVCLDAEHMPLFK 425

RESULT 8
US-09-866-572A-56
; Sequence 56, Application US/09866572A
; Patent No. US20020138859A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacyclases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/866,572A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/457,046
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-866-572A-56

Query Match 6.1%; Score 142; DB 10; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;
QY 5 IQDLTLQGLPGLLSIYTOISILYPSVSSOYPTIVSTFEOGLKRFSEAVPWAGQVKAEG 64
DB 35 LQLSAVDRLPOMKFAFSAVLVYNASSHSIFANPAQIIROALSKVLYQYYPAFAGRIKQE 94
QY 65 ISE-----GNTGTSFIVPFEDVPRVVVKDLRDPDSAPTIEGRKAGYPMAFMFENIIAPR 119
DB 95 NEELEVECTEGALFVEALVNDLSVLRLD-----DAQNASYEQLLF-----136
QY 120 KTLPIGCTGDDPKPVILLQLNFIKGLILITVNGQHGAMDMVGQDAVIRLLSKACRND- 178
DB 137 -SLP--PNIQVQDLHLPLIQVTRTCGGVGVGVGFHGHICDARGTQFLOGLADMARGET 193
QY 179 -PTEEREMTAMNLDKRTIYP-----YLENYTIGPEVDHIOVKADVAGDAVLTPTVSASWAF 233
DB 194 KPLVEPVW-----NRELKPEDLMHLQFHKG--LIRQPLKLD-----EIQOAS 235
QY 234 FTSPKAMSELKDAATKTLDASTKFSVDDALSAFIWKSASRVRLERIDGSAPTFCRAV 293
DB 236 FTINSEIINIYKQC---VIEECNEIFSFAFVVWALTW--IARTKAFQIPHNNVMMFLGM 290
QY 294 DARPAMGVSNYPGLLQNMTHNSTIG-----EIANESLGATASRLRSELDPASM 344
DB 291 DAKRYFN-----PPLPKG--YYGNAIGTSCVNIENQDGLNGSLSRAYMITKSKLIPIEN 343
QY 345 QRTREGLATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSQVD--EIKHENVVGFGRRLGHEFVDFGSG 383

RESULT 10
US-10-166-984-56
; Sequence 56, Application US/10166984
; Publication No. US20040005562A9
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacyclases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 4630-62267
; CURRENT APPLICATION NUMBER: US/10/166,984
; CURRENT FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/866,570

QY 294 DARPAMGVSNYPGLLQNMTHNSTIG-----EIANESLGATASRLRSELDPASM 344
DB 291 DAKRYFN-----PPLPKG--YYGNAIGTSCVNIENQDGLNGSLSRAYMITKSKLIPIEN 343
QY 345 QRTREGLATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSQVD--EIKHENVVGFGRRLGHEFVDFGSG 383

RESULT 9
US-09-866-570A-56
; Sequence 56, Application US/09866570A
; Patent No. US20020168745A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacyclases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/866,570A
; CURRENT FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US/09/457,046B
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-09-866-570A-56

Query Match 5.1%; Score 142; DB 10; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;
QY 5 IQDLTLQGLPGLLSIYTOISILYPSVSSOYPTIVSTFEOGLKRFSEAVPWAGQVKAEG 64
DB 35 LQLSAVDRLPOMKFAFSAVLVYNASSHSIFANPAQIIROALSKVLYQYYPAFAGRIKQE 94
QY 65 ISE-----GNTGTSFIVPFEDVPRVVVKDLRDPDSAPTIEGRKAGYPMAFMFENIIAPR 119
DB 95 NEELEVECTEGALFVEALVNDLSVLRLD-----DAQNASYEQLLF-----136
QY 120 KTLPIGCTGDDPKPVILLQLNFIKGLILITVNGQHGAMDMVGQDAVIRLLSKACRND- 178
DB 137 -SLP--PNIQVQDLHLPLIQVTRTCGGVGVGVGFHGHICDARGTQFLOGLADMARGET 193
QY 179 -PTEEREMTAMNLDKRTIYP-----YLENYTIGPEVDHIOVKADVAGDAVLTPTVSASWAF 233
DB 194 KPLVEPVW-----NRELKPEDLMHLQFHKG--LIRQPLKLD-----EIQOAS 235
QY 234 FTSPKAMSELKDAATKTLDASTKFSVDDALSAFIWKSASRVRLERIDGSAPTFCRAV 293
DB 236 FTINSEIINIYKQC---VIEECNEIFSFAFVVWALTW--IARTKAFQIPHNNVMMFLGM 290
QY 294 DARPAMGVSNYPGLLQNMTHNSTIG-----EIANESLGATASRLRSELDPASM 344
DB 291 DAKRYFN-----PPLPKG--YYGNAIGTSCVNIENQDGLNGSLSRAYMITKSKLIPIEN 343
QY 345 QRTREGLATYIHNNDKSNVSLTADADPSTSVMLSSWAKVGLWDYDFGLG 393
DB 344 LRSRIVA-----NQSQVD--EIKHENVVGFGRRLGHEFVDFGSG 383

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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/457,046
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 09/411,145
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-10-166-984-56

Query Match      6.1%; Score 142; DB 12; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;

QY 5 IQLDTIGQLPGLLSIYTOISLIPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQYKABG 64
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 35 LQLSAVDRLPGMKFATFSAVLVYNASSHSIFANPAQIIRQALSQVLYYPAPAFGRIRQKE 94
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 65 ISE-----GNTGTSFIVPEDPRVVVKLDRDDPSAPTTIEGMRKAGYPMAMPDENIAPR 119
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 95 NEELEVECTGEGALFVEALVNDLSVLRDL-----DAQNASYEQLLF----- 136
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 KTLPIGPGTGPDPKPKVILLQNLFIKGGILLTVNGOHGAMDMVGQDAVIRLLSKACRND- 178
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 137 -SLP--PNTQVQLHLPLILQVTRFTCGGFEVVGFGHHGICDARGGTQFTQGLADMARGET 193
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 -PFTTEEMTAMNLDKRTIYP-----YLENTYITIGPEVDHQIVKADVAGGDAVLTPVSASWAF 233
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 194 KPLVEPVW-----NRELKPEDLMHLQPHKFG--LIRQPLKLD-----EICQAS 235
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 234 FTFSKAMSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAFTFCRAV 293
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 236 FTINSEIINYIKQC---VIEECNEIFSAFEVVVALTW--IARTKAFQIPHENVMMLFGM 290
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 294 DARPAMGVSNYPGLLQNMTHYNSTIG-----EIANESIGATASRLRSELDPASMR 344
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 291 DARKYFN-----PPLPKG--YIGNALGTSVNIENQDILNGSLSRAMVITKSKPILIEN 343
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 345 QRTGRGLATYLHNPNPKSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLG 393
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 344 LRSRIVA-----NQSGVD--EEIKHENVVGFGDMRRLGFEHVDGSG 383
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 12
US-09-866-572A-62
; Sequence 62, Application US/09866572A
; Patent No. US20020138859A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 53679
; CURRENT APPLICATION NUMBER: US/09/866,572A
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: 09/457,046
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 62
; LENGTH: 436
; TYPE: PRT
; ORGANISM: Arabidopsis thaliana
US-09-866-572A-62

Query Match      6.1%; Score 141.5; DB 10; Length 436;
Best Local Similarity 22.2%; Pred. No. 5.5e-05;
Matches 74; Conservative 56; Mismatches 133; Indels 71; Gaps 14;

QY 135 PVILLQNLFIK--GGLILTVNGOHGAMDMVGQDAVIRLLSKACRN-----DPFTE----- 182
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Db 135 PVLLIQANFPSCGLVITTCVSHKITDATSLAMFIRGWAESSRGLGILITLIPSTASVFP 194
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 183 ---EEMTAMNLDKRTIYPYLENTYITIGPEVDHQIVKADVAGGDAVLTPVSASWAF 239
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 195 KPLDELPSKPMDRK-----EEVEE-----MSCVTXRFVFDAS 226
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 240 AMSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAFTFCRAVDARFAM 299
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 227 KIKKLAKASRNL---VKNPTRVEAVTALFWRCVTKV--SELSLIP-----RTSVLQILV 277
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 300 GVSNNYPGLLQNMTHYNSTIGETAINBSLGATASRLRSELDPASMRQTRGLATYLHNPD 359
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 278 NLRGKVDLSLCTIGNMLSLMLKNEE--AAIERIQDVVDEI---RAKEIFSLNCKEMS 332
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 360 KSNVSLTADADPSTV-----MLSSWAKVGLMDYDFGLGKPEVTRRPIPEPVE 409
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Db 333 KSSSRIFELLEETGKYVGRGNEMDLWMSNCKGLGYDADF--GWGKPVVWVTRGTSHF 390
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; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/457,046
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 09/411,145
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-10-166-984-56

Query Match      6.1%; Score 142; DB 15; Length 448;
Best Local Similarity 20.5%; Pred. No. 5.1e-05;
Matches 84; Conservative 61; Mismatches 184; Indels 80; Gaps 16;

QY 5 IQLDTIGQLPGLLSIYTOISLIPVSDSSQYPTIVSTFEQGLKRFSEAVPWVAGQYKABG 64
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Db 35 LQLSAVDRLPGMKFATFSAVLVYNASSHSIFANPAQIIRQALSQVLYYPAPAFGRIRQKE 94
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QY 65 ISE-----GNTGTSFIVPEDPRVVVKLDRDDPSAPTTIEGMRKAGYPMAMPDENIAPR 119
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Db 95 NEELEVECTGEGALFVEALVNDLSVLRDL-----DAQNASYEQLLF----- 136
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 120 KTLPIGPGTGPDPKPKVILLQNLFIKGGILLTVNGOHGAMDMVGQDAVIRLLSKACRND- 178
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 137 -SLP--PNTQVQLHLPLILQVTRFTCGGFEVVGFGHHGICDARGGTQFTQGLADMARGET 193
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 179 -PFTTEEMTAMNLDKRTIYP-----YLENTYITIGPEVDHQIVKADVAGGDAVLTPVSASWAF 233
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 194 KPLVEPVW-----NRELKPEDLMHLQPHKFG--LIRQPLKLD-----EICQAS 235
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 234 FTFSKAMSELKDAATKTLDASTKFTVSTDDALSFTWKSASRVRLERIDGSAFTFCRAV 293
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 236 FTINSEIINYIKQC---VIEECNEIFSAFEVVVALTW--IARTKAFQIPHENVMMLFGM 290
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 294 DARPAMGVSNYPGLLQNMTHYNSTIG-----EIANESIGATASRLRSELDPASMR 344
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 291 DARKYFN-----PPLPKG--YIGNALGTSVNIENQDILNGSLSRAMVITKSKPILIEN 343
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
QY 345 QRTGRGLATYLHNPNPKSNVSLTADADPSTSVMLSSWAKVGLMDYDFGLG 393
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:
Db 344 LRSRIVA-----NQSGVD--EEIKHENVVGFGDMRRLGFEHVDGSG 383
   :||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:||||:

RESULT 11
US-10-166-984-56
; Sequence 56, Application US/10166984
; Publication No. US20030108891A1
; GENERAL INFORMATION:
; APPLICANT: Croteau, Rodney et al.
; TITLE OF INVENTION: Transacylases of the Paclitaxel Biosynthetic Pathway
; FILE REFERENCE: 4630-62267
; CURRENT APPLICATION NUMBER: US/10/166,984
; PRIOR FILING DATE: 2002-06-10
; PRIOR APPLICATION NUMBER: US 09/866,570
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/457,046
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 09/411,145
; PRIOR FILING DATE: 1999-09-30
; NUMBER OF SEQ ID NOS: 76
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 56
; LENGTH: 448
; TYPE: PRT
; ORGANISM: Taxus cuspidata
US-10-166-984-56
```


[illegible]

Db 227 KIKKLAKASRNL-----VKNPTRVEAVTALFWRCVTKV--SRLSSLTP-----RTSVLIQILV 277

Qy 300 GVSNNYPGLLQNMTHNSTIGEIANESLGATASRLRSELDPASMRQRTFGLATYLYLHNP 359

Db 278 NLRGKVDLSICENTIGNMLSLMILKNEE--AAIERIQDVVDEI---RRAKEIFSLNCKEMS 332

Qy 360 KSNVSLTADADPSTV-----MLSSWAKVGLWDYDFGLGLGKPKETVRRPIPEPVE 409

Db 333 KSSSRIFELLEIEIGKVYGRGNEMDLWMSNSWCKLGLYDADF--GWGKPVWVTGRTGTSHEK 390

Qy 410 SLMYFMPKKPDGEFCFAA-LSLRDEMDRLKADKE 442

Db 391 NLMLLIDTK-DGEGIEAWITLTTEEQMSLFECDQE 423

Search completed: February 8, 2004, 00:12:21

Job time : 249 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 18:04:23 ; Search time 3189 Seconds

(without alignments)
10334.547 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggcttcaagatacagct.....atggcagtagcttggttag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST.*

1: em_estba.*

2: em_esthum.*

3: em_estin.*

4: em_estm.*

5: em_estov.*

6: em_estpl.*

7: em_estro.*

8: em_htc.*

9: gb_est1.*

10: gb_est2.*

11: gb_htc.*

12: gb_est3.*

13: gb_est4.*

14: gb_est5.*

15: em_estfun.*

16: em_estom.*

17: em_gss_hum.*

18: em_gss_inv.*

19: em_gss_pln.*

20: em_gss_vrt.*

21: em_gss_fun.*

22: em_gss_mam.*

23: em_gss_mus.*

24: em_gss_pro.*

25: em_gss_rod.*

26: em_gss_phg.*

27: em_gss_vrl.*

28: gb_gss1.*

29: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663.8	49.0	899	12	BI949616
2	406	29.9	1055	12	BI947129
3	354.2	26.1	512	12	BI191800
4	351	25.9	508	12	BI191865

5	323.4	23.8	498	12	BI200717
6	317.6	23.4	499	12	BI191678
7	296.6	21.9	481	12	BI191864
8	278.4	20.5	514	12	BI192008
9	278	20.5	411	12	BI187781
10	273.4	20.2	448	12	BI201068
11	273	20.1	518	12	BI191997
12	268.4	19.8	457	12	BI187780
13	258	19.0	392	12	BI192452
14	254.8	18.5	423	12	BI192498
15	251.2	18.5	490	12	BI201353
16	247.4	18.2	374	12	BI187896
17	242.8	17.9	476	12	BI182381
18	234.4	17.3	401	12	BI188598
19	234.4	17.3	401	12	BI192451
20	233.4	17.2	348	12	BI191129
21	231.6	17.1	459	12	BI187539
22	231.2	17.1	393	12	BI188605
23	226.6	16.7	372	12	BI192380
24	223.8	16.5	336	12	BI191040
25	218.6	16.1	358	12	BI201146
26	217.2	16.0	435	12	BI187304
27	215.4	15.9	350	12	BI190499
28	206.6	15.2	330	12	BI191128
29	202	14.9	546	10	BF253868
30	196	14.5	385	12	BI189867
31	195	14.4	318	12	BI192335
32	187.6	13.8	303	12	BI188705
33	187.6	13.8	303	12	BI189964
34	187.6	13.8	304	12	BI190847
35	187.6	13.8	308	12	BI188363
36	187.6	13.8	308	12	BI190145
37	187	13.8	311	12	BI200611
38	170.4	12.6	373	12	BI190682
39	170.4	12.6	376	12	BI189442
40	170.4	12.6	380	12	BI190409
41	169.4	12.5	352	12	BI188631
42	169.4	12.5	352	12	BI201565
43	169.4	12.5	360	12	BI187939
44	169.4	12.5	361	12	BI201147
45	169.4	12.5	379	12	BI189968

ALIGNMENTS

RESULT 1
BI949616
LOCUS
DEFINITION
BI949616
HVSME10014017f Hordeum vulgare spike EST library HVCN0012
(Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME10014017f, mRNA sequence.

ACCESSION
BI949616
VERSION
BI949616.1
KEYWORDS
EST.
SOURCE
Hordeum vulgare subsp. vulgare
ORGANISM
Hordeum vulgare subsp. vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae
; Triticeae; Hordeum.
REFERENCE
1 (bases 1 to 899)
Wing,R., Muehlbauer,G.J., Close,T.J., Kleinhofs,A., Wise,R., Heinen
S., Begum,D., Frisch,D., Yu,Y., Henry,D., Palmer,M., Rambo,T.,
Simmons,J., Fenton,R.D., Malatrasi,M., Choi,D.W., Oates,R. and Main
D.
Development of a genetically and physically anchored EST resource
for barley genomics: Fusarium infected Morex spike cDNA library
Unpublished
Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288

Fax: 864 656 4293
Email: rwing@clermson.edu
Total hq bases = 598
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence stop: 755.
Location/Qualifiers
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/tissue_type="Spike"
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/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab; spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the RJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"
BASE COUNT 223 a 262 c 204 g 209 t 1 others
ORIGIN

Query Match 49.0%; Score 663.8; DB 12; Length 899;
Best Local Similarity 95.8%; Pred. No. 6.9e-178;
Matches 724; Conservative 0; Mismatches 28; Indels 4; Gaps 4;
QY 1 ATGGCTTCAAGATACAGCTCGACACCTCGGCAGCTACGAGGCTCTTTCGATCTAC 60
DB 110 ATGGCTTCAAGATACAGCTCGACACCTCGGCAGCTACGAGGCTCTTTCGATCTAC 169
QY 61 ACCCAATCAGTCTCTTACCCCGTCTCGATTCCTCAATATCCCAATATGTGTCAGC 120
DB 170 ACCCAATCAGTCTCTTACCCCGTCTCGATTCCTCAATATCCCAATATGTGTCAGC 229
QY 121 ACCTTCGAGCAAGTCTTAAGCGGTTCTCGAAGCGCTCCCATCGGTCGAGCGCAGGTC 180
DB 230 ACCTTCGAGCAAGTCTTAAGCGGTTCTCGAAGCGCTCCCATCGGTCGAGCGCAGGTC 289
QY 181 AAGCCGAGGCGATTACGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC 240
DB 290 AAGCCGAGGCGATTACGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGAC 349
QY 241 GTTCTCTGTTGTAGTGAAGACCTCCGGATGATCTTTTCAGCGCCACGATCGAGGGT 300
DB 350 GTTCTCTGTTGTAGTGAAGACCTCCGGATGATCTTTTCAGCAACCCAGATCGAGGGT 409
QY 301 ATGAGAAGCGGGGATACCTTATGGCGATGTTTTCAGAGAACATCATCGCGCCAGGAAG 360
DB 410 ATGAGAAGCGGGGATACCTTATGGCGATGTTTTCAGAGAACATCATCGCGCCAGGAAG 469

QY 361 ACGTTACCTATTGGACCTGGTACTCCCGACGACCCAAAGCCCTGTAAATTCATTGGCAG 420
DB |||||
QY 470 ACGTTACCTATTGGACCTGGTACTCCCGACGACCCAAAGCCCTGTAAATTCATTGGCAG 529
DB |||||
QY 421 CTCAACTTCATCAAGGGCGGACTCATCTCACTGTCAACGGACAGCAGCTGCTATGGAT 480
DB |||||
QY 530 CTCAACTTCATCAAGGGCGGACTCATCTCACTGTCAACGGACAGCAGCTGCTATGGAT 589
DB |||||
QY 481 ATGGTAGGCCAAGATCGGCTGATCGTCTACTCTCTCAAGGCGTCCGTAACGACCCATTC 540
DB |||||
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DB |||||
QY 541 ACCGAAGAGGAATGACGCCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGA 600
DB |||||
QY 650 ACCGAAGAGGAATGACGCCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGA 708
DB |||||
QY 601 AACTATACGATTGGCCCCGAGGTAGATCATCATGATGTCAAAGCTGATAGTGTGTT 660
DB |||||
QY 709 AACTATACGATTGGCCCCGAGGTAGATCATCATGATGTCAAAGCTGATAGTGTGTT 768
DB |||||
QY 661 GACGCTGT-TCTCAGCGCGTCAAGCTGCAAGCTGGCGGTTCTTCAATTGAGCCCAAGGC 719
DB |||||
QY 769 GTGACGCTGTCTCACCCCGTCAAGCTGCGAGCTGGGCGCTTTCACATTCAGCCCC-AGGC 827
DB |||||
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DB |||||
QY 828 CATGTCANAGCTC-AGGATGCTGTACCAAGAACTCT 862
DB |||||
BI947129 1055 bp mRNA linear EST 19-OCT-2001
HVSME1003N10f Hordeum vulgare spike EST library HVCDNA0012
DEFINITION (Fusarium infected) Hordeum vulgare subsp. vulgare cDNA clone
HVSME1003N10f, mRNA sequence.
ACCESSION BI947129
VERSION BI947129.1 GI:16286403
KEYWORDS Hordeum vulgare subsp. vulgare
SOURCE Hordeum vulgare subsp. vulgare
ORGANISM Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
REFERENCE 1 (bases 1 to 1055)
AUTHORS Wing, R., Muehlbauer, G.J., Close, T.J., Kleinhofs, A., Wise, R., Heinen, S., Begum, D., Frisch, D., Yu, Y., Henry, D., Palmer, M., Rambo, T., Simmons, J., Fenton, R.D., Malatrasi, M., Choi, D.W., Oates, R. and Main, D.
TITLE Development of a genetically and physically anchored EST resource for barley genomics: Fusarium infected Morex spike cDNA library
JOURNAL Unpublished
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
Total hq bases = 147
Seq primer: AATTAAACCTCACTAAAGGG
High quality sequence start: 5
High quality sequence stop: 668.
Location/Qualifiers
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/clone_lib="Hordeum vulgare spike EST library HVCDNA0012 (Fusarium infected)"

/note="Vector: pBluescript SK(-); Site 1: EcoRI; Site 2: XhoI; Plants were grown at the University of Minnesota in the GJ Muehlbauer lab, spikes were harvested and snap frozen at 0, 1, 2, 3, 4, 5, 6, and 8 days after Fusarium graminearum inoculation (Heinen). In the TJ Close lab at the University of California, Riverside, total RNA was prepared from each sample pool, equal quantities of all eight RNA pools were combined, poly(A) RNA was purified from the mixture, one primary unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi, Fenton, Malatrasi). Phagemids were plated and picked at the Clemson University Genomics Institute (CUGI) (Begum, Palmer, Frisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Frisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence and contains a minimum of 100 bases of phred value 20 or above. For more details on library preparation and sequence analysis see <http://www.genome.clemson.edu/projects/barley>. To order this clone see <http://www.genome.clemson.edu/orders> Also see Close TJ, Wing R, Kleinhofs A, Wise R (2001) Genetically and physically anchored EST resources for barley genomics. Barley Genetics Newsletter 31:29-30. (<http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html>)"

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BASE COUNT      300 a 313 c 227 g 215 t
ORIGIN
Query Match      29.9%; Score 406; DB 12; Length 1055;
Best Local Similarity 79.4%; Pred. No. 2.4e-104;
Matches 481; Conservative 0; Mismatches 125; Indels 0; Gaps 0;

QY 387 TCCGAGACCCAAAGCTGTAATTCATTTCAGCTCAACTTCATCAAGGCGGACTCAT 446
Db 1 TCCGAGACCCAAAGCTGTAATTCATTTCAGCTCAACTTCATCAAGGCGGACTCAT 60

QY 447 CCTCACTGTCAACGACGACGCTGTATGGATATGGTAGGCAAGATGGCGTATCCG 506
Db 61 GCTCACTGTCAACGACGACGCTGTATGGATATGGTAGGCAAGATGGCGTATCCG 120

QY 507 TCTACTCTCAAGCGCTGCCGTACGACCCATTCACCGAAGAGAAATGACGGCCATGAA 566
Db 121 TCTACTCTCAAGCGCTGCCGTACGACCCATTCACCGAAGAGAAATGACGGCCATGAA 180

QY 567 CCTCGATCGCAAGCAGTAGTTCCTTACCTTGAAATATACAGATGGCCCCGAGGTAGA 626
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QY 627 TCATCAGATTGTCAAAGCTGATGTAGCTGGTGGTGACGCTGTTCTACGCGGGTCAGTGC 686
Db 241 TCATCAGATTGTCAAAGCTGATGTAGCTGGTGGTGACGCTGTTCTACGCGGGTCAGTGC 300

QY 687 AAGCTGGCGCTTCTTCAATTCAGCCCAAGGCCATGTACAGCTCAAGGATGTGCTAC 746
Db 301 AAGCTGGCGCTTCTTCAATTCAGCCCAAGGCCATGTACAGCTCAAGGATGTGCTAC 360

QY 747 CAAGACTCTTGACGATCAACAAGTTCGTGTGACAGTGCTCTTTTCGGCGTTTCAT 806
Db 361 CAAGAAATTTTACGCAATTAACAAGTTTCGTGTGACAGTGCTCTTTTCGGCGTTTCAT 420

QY 807 CTGGAATCGGCTCTCGCGTGGCTTCGAAAGAAATCGATGGCTCTGCACCTACCGAGTT 866
Db 421 CTGGAATCGGCTCTCGCGTGGCTTCGAAAGAAATCGATGGCTCTGCACCTACCGAGTT 480

QY 867 CTCGGCTGTGTTGATGCTCGACGGCAATGGGTGTCTCGAAACAATACCGAGCGCTTCT 926
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QY 927 TCAAAACATGACCTACCAACATCTGCACCATTCGGCGAAATCCGCAACAGAGTCACTCGGCGC 986
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QY 987 AACAGC 992
Db 601 ACCAGC 606

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RESULT 3 BI191800

LOCUS
DEFINITION

BI191800 512 bp mRNA linear EST 10-JUL-2001
12f11fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
library Fusarium sporotrichioides cDNA clone 12f11fs 5', mRNA
sequence.

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

Other ESTs: 12f11fs.f1
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
871 8e-94 gi|437882|gb|ARD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
High quality sequence stop: 476.

FEATURES

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XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
; 3' end of cDNA cloned into XhoI site of pBluescript"
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Best Local Similarity 82.8%; Pred. No. 8.8e-90;
Matches 407; Conservative 0; Mismatches 88; Indels 0; Gaps 0;

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Db 76 CCAGATCAGTCTCGTTTACCCCGTCTCTGATTCCTCTCCAGTATCCCACTATCTCAGCAC 135

QY 123 CTTTCGAGCAGGCTCTTAAGCGTTCCTCCGAGCCGTCCTCATGGTTCGAGGCGAGTCAA 182
Db 136 CTTTCGAGGAGCGCTTAAACCGCTCTCTCAACCTTCCCATGGTTCGCGGCGAGTCAA 195

QY 183 AGCCGAGGAGCATTTAGCGAGGGAACACAGAACTTCTTTCGTCCTTTTTCAGACGT 242
Db 196 GACCGAGGAGCATTCAGCGAAGGAACACAGAACTTCTTTCAGATCATTTCCATATGAGGAGAC 255

QY 243 TCTCGTGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGCGGCCCACTGATCGAGGTAT 302

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Db	73	CCAGATCAGTCTCTGTTTACCCCGTCTCTGATTCCTCTCCAGTATCCACCATCGTCAGCAC	132
Qy	123	CTTCGAGCAAGTCTTTAAGCGCTTCTCGAAGCCGCTCCATGGTTCGAGGCCAGGTCAA	182
Db	133	CTTTCGAGGAAGCCCTAAAGCGCTCTGTCAAACTTCCCATGGTTCGGGGCCAGGTCAA	192
Qy	183	AGCCGAGGGCATTACGAGGGGAAACACAGGAACCTTCTTATCTGCTCCCTTTTGGAGACGT	242
Db	193	GACCGAGGGCATCAGCGAAGGAGACACAGGAACCTTCCAAAGATCATTCATATGAGAGAC	252
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Qy	303	GAGAAAGCGGGATACCCCTATGGCGATGTTTTCAGGAGAACATCATCGCCCAAGGAGAC	362
Db	313	GAGAAAGCGGGTTCCTCCCTTAGAGATGTTTTCAGGAGAACCTTCGTCGCTCCGAGGAAGAC	372
Qy	363	GTCTACTATTGACACCTGGTACTGTCCTCCGACGACCCAAAGCCCTGTAATTTCTATTGAGCT	422
Db	373	ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCCAAGCCCTGTTGTTATTGAGCT	432
Qy	423	CAACTTCATCAAGGGCGGACTCATCTCTCACTGTCTCAACGAGCAGACGGTGTATGATAT	482
Db	433	CAACTTCATTAAGGGCGGACTCATCTCTCACTGTCTCAACGAGCAGACGGTGTATGATAT	492
Qy	483	GGTAGCCCAAGATGC	497
Db	493	GACAGGACCAAGATGC	507
RESULT 5			
BI191865	508 bp	mrna	linear
LOCUS	EST 10-JUL-2001		
DEFINITION	13b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone 13b10fs 5', mRNA		
ACCESSION	BI191865		
VERSION	BI191865.1	GI:14665544	
KEYWORDS	EST.		
SOURCE	Fusarium sporotrichioides		
ORGANISM	Fusarium sporotrichioides		
REFERENCE	1 (bases 1 to 508)		
AUTHORS	Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand,M. and Roe,B.		
TITLE	Analysis of a Fusarium sporotrichioides EST database		
JOURNAL	Unpublished		
COMMENT	Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu Department of Chemistry and Biochemistry Advanced Center for Genome Technology, University of Oklahoma 620 Farrington Oval, Norman, OK 73019, USA Tel: 405 325 4912 Fax: 405 325 7762 Email: broe@ou.edu Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01 857 3e-92 gi 4378882 gb AAD197 (AF127176) trichothecene3-O-acetyltransfer Seq primer: T3 High quality sequence stop: 450.		
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	/clone="13b10fs"		
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	/note="vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"		
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ORIGIN			
Query Match	25.9%; Score 351; DB 12; Length 508;		
Best Local Similarity	81.8%; Pred.No. 7.2e-89;		
Matches 405; Conservative	0; Mismatches 90; Indels 0; Gaps 0;		
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Db      475 ATTAGTATCGGACCTGGCAATGGCCCAACGACCCGAAG 514

RESULT 9
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DEFINITION b2d04fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
            library Fusarium sporotrichioides cDNA clone b2d04fs 5', mRNA
            sequence.
ACCESSION Bi187781
VERSION    Bi187781.1 GI:14661460
KEYWORDS   EST.
SOURCE     Fusarium sporotrichioides
ORGANISM   Fusarium sporotrichioides
REFERENCE  1 (bases 1 to 411)
AUTHORS    Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
            ,M. and Roe,B.
TITLE      Analysis of a Fusarium sporotrichioides EST database
JOURNAL    Unpublished
COMMENT    Other ESTs: b2d04fs.f1
            Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            Contact Dr. Marian Beremand regarding clone availability Included
            is the best homolog from a blastx search of Genbank nr 04-09-01
            591 4e-61 gi|4378882|gb|AAD197 (AF127176)
            trichothecene3-O-acetyltransfer
            Seq primer: T3
            High quality sequence stop: 307.
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     cDNA library"
     notes="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
     XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
     XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT          99 a 122 c 96 g 94 t
ORIGIN
Query Match      20.5%; Score 278; DB 12; Length 411;
Best Local Similarity 81.2%; Pred. No. 4.1e-68;
Matches 336; Conservative 0; Mismatches 75; Indels 3; Gaps 1;

QY      401 AGCCTGTAATTCATTGACGCTCAACTTCATCAAGGCGGACTCATCTCACTGTCAAG 460
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Db      1 AGCCTGTGTTGCTATTGCACTCAACTTCATTAAAGCGGACTCATCTCACTGTCAAG 60
         |||||||

QY      461 GACAGCAGGTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 520
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Db      61 GACAAATGTTGCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 120
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QY      521 CGTGGCGTAACGACCCATTACCGAGAGAGAAATGACGGCGATGAACCTCGATCGCAAGA 580
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QY      581 CGATAGTTCCTTACCTTGAAATCTATACAGTTGCGCCCGAGGTAGATCATCAGATGTCTA 640
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QY      641 AAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 700
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QY      761 CATCAACAAGATTCGTTCGACTGACGATGCTCTTTCGGCGTTTCATCTGGAAT 814
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RESULT 10
Bi201068/c
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DEFINITION O4C12fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
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            sequence.
ACCESSION Bi201068
VERSION    Bi201068.1 GI:14667040
KEYWORDS   EST.
SOURCE     Fusarium sporotrichioides
ORGANISM   Fusarium sporotrichioides
REFERENCE  1 (bases 1 to 448)
AUTHORS    Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
            ,M. and Roe,B.
TITLE      Analysis of a Fusarium sporotrichioides EST database
JOURNAL    Unpublished
COMMENT    Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
            Department of Chemistry and Biochemistry
            Advanced Center for Genome Technology, University of Oklahoma
            620 Parrington Oval, Norman, OK 73019, USA
            Tel: 405 325 4912
            Fax: 405 325 7762
            Email: broe@ou.edu
            Contact Dr. Marian Beremand regarding clone availability Included
            is the best homolog from a blastx search of Genbank nr 04-09-01
            694 4e-73 gi|4378882|gb|AAD197 (AF127176)
            trichothecene3-O-acetyltransfer
            Seq primer: M13-20
            High quality sequence stop: 303.
FEATURES             Location/Qualifiers
     source           1..448
     mol_type="mRNA"
     strain="Tri 10"
     db_xref="taxon:5514"
     clone="o4c12fs"
     clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
     cDNA library"
     notes="vector: pBluescript SK-; Site 1: EcoRI; Site 2:
     XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
     XhoI; 3' end of cDNA cloned into XhoI site of pBluescript"
BASE COUNT          107 a 126 c 101 g 114 t
ORIGIN
Query Match      20.2%; Score 273.4; DB 12; Length 448;
Best Local Similarity 79.9%; Pred. No. 8.8e-67;
Matches 322; Conservative 0; Mismatches 81; Indels 0; Gaps 0;

QY      954 CATCGCGGAATCGCAACGAGTCACTCGCGCAACAGCATACGCTTCGTTTCAAGACT 1013
         |||||||
Db      448 CGTTCGCGGAATCGCAACGAGTCACTTCGCGCAACAGCATACGCTTCGCTCGGAAT 389
         |||||||

QY      1014 CGACCCCGCGGATCGCGCGAGCAAGAGTCTCGCGACGTACTGACACAAACCC 1073
         |||||||
Db      388 CAACAGTATCGTTTCGCGAGCAACAAAGCTTTGGCGAGCTATCATGCGCTGCC 329
         |||||||

QY      1074 CGACAAGTCAACGATATCCTGACGGCTGATCGGACCCATCTACCAGCGTCAATGCTGAG 1133
         |||||||
Db      328 TGAAGTTCGAGGCTCTCCCTGACCGCGGATCGGATCGTCAAGCAGCATCATGCTGAG 269
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QY      1134 TTCTTGGCGCAAGGTGGGACTCTGGGATTCAGACTTTTGGGCTCGGACTGGTAAAGCCGA 1193
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268 TTCTGGCCAGAGTGGGATGCTGGAGTATGACTTTGGTTGGAGTGGTAAAGCTGA 209
 1194 GACTGTGAGACGGCCAACTTTGAGCTCTTGAGAGCTTGATGTTATGATGCCAAGAA 1253
 208 GAGTGTGAGAGACCTCGCTTTGAACTTTGAGAGTTTGATGTTATGATGCCAAGAA 149
 1254 GCGTATGCGAGTCTGTGCGGCGCTTTCTCTGAGGATGAGGATGAGCAGATTGAA 1313
 148 GCGTATGCGGAGTTTACCGCGTCCATTTCTCTGAGGATGAGGATGAGGAGACTAAA 89
 1314 GCGGATAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
 88 GCGGATAGGAGTGGACCAAGTATGCGCAGTATGTTGGTAG 46

RESULT 11

BI191997
 LOCUS
 DEFINITION
 14b10fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone 14b10fs 5', mRNA
 sequence.

ACCESSION

BI191997

VERSION

BI191997.1 GI:14665676

KEYWORDS

EST.

SOURCE

Fusarium sporotrichioides

ORGANISM

Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 1 (bases 1 to 518)

REFERENCE

Ren.Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
 M. and Roe,B.
 Analysis of a Fusarium sporotrichioides EST database
 Unpublished

TITLE

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

JOURNAL

Department of Chemistry and Biochemistry

COMMENT

Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability Included
 is the best homolog from a blastx search of Genbank nr 04-09-01
 712 3e-75 gi|4378882|gb|AAD197 (AF127176)
 trichothecene3-O-acetyltransfer
 Seq primer: T3
 High quality sequence stop: 484.

FEATURES

source

1. .518
 Location/Qualifiers
 /organism="Fusarium sporotrichioides"
 /mol_type="mRNA"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="14b10fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"
 137 a 162 c 112 g 107 t

BASE COUNT

ORIGIN

Query Match 20.1%; Score 273; DB 12; Length 518;
 Best Local Similarity 80.9%; Pred. No. 1.2e-66;
 Matches 318; Conservative 0; Mismatches 75; Indels 0; Gaps 0;
 3 GGCTTTCAAGATACAGTTCGACACCTCGCGGAGTACCGAGTCCCTTTGATCTACAC 62
 126 GTCTTTTGACATAGAGTTCGACATCATCGCCAGCAACCGCTCTTCTTCAATCTAC 185
 63 CCAATCAGTCTCTCTACCCCGTCTGATCTCTCTCAATATCCGACTATTGTCAGAC 122
 186 CCAGATCAGTCTCGTTTACCCCGTCTGATCTCTCGGATCCCGACCATCGTCAGAC 245

123 CTTGAGCAAGGCTTTAAGCGCTTCTCCGAAGCCCTCCCATGGTGCAGGCCAGGTCAA 182
 246 CTTGAGGAGGAGGCTTAAACGGCTCTCTCAAACCTTCCCATGGTGCAGGCCAGGTCAA 305
 183 ACCGAGGGCATAGGAGGGGAAACACAGGAATCTTCCTTTATCGTCCCTTTTGAGGACGT 242
 306 GACCGAGGGCATCAGCGAGGAAACACAGGAATCTTCCAAAGATCATTCATATGAGGAGAC 365
 243 TCCTCGTGTGTAGTCAAGACCTCCGCGATGATCTTCAGCGCCCAAGCATCAGGGTAT 302
 366 ACCCGTCTTGTGGTAAAGACCTCCGTGATGATTCCTCAGCGCCCAAGCATCAGGGTAT 425
 303 GAGAAAGCGGGATACCTTATGCGGATGTTTTCAGGAGAAACATATCGCCCAAGGAGAC 362
 426 GAGAAAGCGGGTTCCTCCCTTAGAGATGTTTTCAGGAGAAACGTGCTCGGAGGAGAC 485
 363 GTTACTATTGACCTGGTACTGTCCTCCGACGA 395
 486 ATTAGCTATCGGACCTGGCAATGGCCCAACGA 518

RESULT 12

BI187780/c

LOCUS

BI187780

DEFINITION

457 bp mRNA linear EST 10-JUL-2001
 b2d04fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
 library Fusarium sporotrichioides cDNA clone b2d04fs 3', mRNA
 sequence.

ACCESSION

BI187780

VERSION

BI187780.1 GI:14661459

KEYWORDS

EST.

SOURCE

Fusarium sporotrichioides

ORGANISM

Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
 Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 1 (bases 1 to 457)

REFERENCE

Ren.Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand

M. and Roe,B.

Analysis of a Fusarium sporotrichioides EST database

Unpublished

Other ESTs: b2d04fs.r1

Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu

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Advanced Center for Genome Technology, University of Oklahoma

620 Parrington Oval, Norman, OK 73019, USA

Tel: 405 325 4912

Fax: 405 325 7762

Email: broe@ou.edu

Contact Dr. Marian Beremand regarding clone availability Included

is the best homolog from a blastx search of Genbank nr 04-09-01

655 5e-70 gi|4378882|gb|AAD197 (AF127176)

trichothecene3-O-acetyltransfer

Seq primer: M13-20

High quality sequence stop: 257.

FEATURES

source

1. .457
 Location/Qualifiers
 /organism="Fusarium sporotrichioides"
 /mol_type="mRNA"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="b2d04fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed
 cDNA library"
 /note="Vector: pBluescript SK-; Site 1: EcoRI; Site 2:
 XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript
 ; 3' end of cDNA cloned into XhoI site of pBluescript"
 109 a 128 c 104 g 116 t

BASE COUNT

ORIGIN

Query Match 19.8%; Score 268.4; DB 12; Length 457;
 Best Local Similarity 80.0%; Pred. No. 2.4e-65;
 Matches 328; Conservative 0; Mismatches 81; Indels 1; Gaps 1;

QY 947 ACTCGACCATCGCGAATCGCAACAGTCACTCGGCGCAACAGCATCAACGCTTCGTT 1006
 Db |||||
 QY 454 ACTCGACCGTCCCGAATCGCAACGA-ACCTTGGCGCAACAGCATCACGCTCGCGT 396
 Db |||||
 QY 1007 CAGAACTGACCCCGGAGCATCGCCAGCGCAACAGAGGTCTCGCGAGTACCTGCACA 1066
 Db |||||
 QY 395 CGAACTCAACAGTCACTCGTTGGCGAGAGCAACAGCTTTGGCGAGTACATGCATG 336
 Db |||||
 QY 1067 ACAACCCGACAGTCCCAACGATCCCTGACGGCTGATGCGGACCACTACCGAGTCA 1126
 Db |||||
 QY 335 GCCTGCTGACAAAGTCGAGCGTCTCCCTGACCGCGATCGGAATCCGTCAAGCAGCATCA 276
 Db |||||
 QY 1127 TGCTGAGTCTTTGGCCCAAGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTA 1186
 Db |||||
 QY 275 TGCTGAGTCTCGGCGCAAGTGGGATGCTGGAGTATGACTTTGGGTTGGACTGGGTA 216
 Db |||||
 QY 1187 AGCCGAGACTGTGAGACGGGCAATCTTTGAGCCCTGTTGAGACTTGTATGTTATATGC 1246
 Db |||||
 QY 215 AGCCTGAGAGTGTGAGAGACCTCGCTTTGAACCTTTTGAGAGTTTGAATGTTATATGC 156
 Db |||||
 QY 1247 CCAAGAAGCCTGATGCGGAGTCTGTGCGGCGCTTCTCTGAGGATGAGGATATGGACC 1306
 Db |||||
 QY 155 CCAAGAAGCCTGATGCGGAGTCTGTGCGGCGCTTCTCTGAGGATGAGGATATGGAGA 96
 Db |||||
 QY 1307 GATTGAAGCGGATGAAGAGTGGACCAAGTATGCGCAGTACGTTGCTTTAG 1356
 Db |||||
 QY 95 GACTAAAGCGGATGAGAGTGGACAAAGTACGCAAGTATATTGGGTAG 46
 Db |||||

RESULT 13
 B1192452
 LOCUS
 DEFINITION
 m4b09fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone m4b09fs 5', mRNA sequence.

ACCESSION
 B1192452
 VERSION
 B1192452.1 GI:14666131
 KEYWORDS
 EST.
 SOURCE
 Fusarium sporotrichioides
 ORGANISM
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 REFERENCE
 1 (bases 1 to 392)
 Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand M. and Roe,B.
 TITLE
 Analysis of a Fusarium sporotrichioides EST database
 JOURNAL
 Unpublished
 COMMENT
 Other ESTs: m4b09fs.f1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01
 557 3e-57 gi|437882|gb|AAD197 (AF127176)
 trichothecene3-O-acetyltransferase
 Seq primer: T3
 High quality sequence stop: 361.

FEATURES
 source
 1..392
 Location/Qualifiers
 /organism="Fusarium sporotrichioides"
 /mol_type="mRNA"
 /strain="Tri 10"
 /db_xref="taxon:5514"
 /clone="m4b09fs"
 /clone_lib="Fusarium sporotrichioides Tri 10 overexpressed cDNA library"
 /notes="Vector: pBluescript SK-; Site 1: EcoRI; Site 2: XhoI; 5' end of cDNA cloned into EcoRI site of pBluescript ; 3' end of cDNA cloned into XhoI site of pBluescript"

BASE COUNT 98 a 121 c 92 g 81 t
 ORIGIN
 Query Match 19.0%; Score 258; DB 12; Length 392;
 Best Local Similarity 80.2%; Pred. No. 2e-62; Indels 3; Gaps 1;
 Matches 316; Conservative 0; Mismatches 0
 QY 347 TCGCCCAAGGAGACGTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGCCCTG 406
 Db |||||
 QY 1 TCGCTCCGAGGAAGACATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGCCCTG 60
 Db |||||
 QY 407 TAAATTCATTCAGCTCAACTTCATCAAGGGGGAGCATCATCTCTACTGTCAACGACAGC 466
 Db |||||
 QY 61 TGTGTCTATTGAGCTCAACTTCATTAAGGGGGGAGTCACTTCTCAACCGTCAACGACAAAC 120
 Db |||||
 QY 467 ACGGTGCTATGATGATGATGAGCCAAAGATGCGGTGATCCGCTCTACTCTCCAGGCGTGC 526
 Db |||||
 QY 121 ATGGTGTCTATGACATGACAGACCAAGATGAATATTTCGTCCTCTCCAGGCGTGC 180
 Db |||||
 QY 527 GTAAGCAACCAATTCACCGAAGAGGAATGACGGCCATGAACCTCGATCGCAAGACGATAG 586
 Db |||||
 QY 181 CCAACGAATATTTCACCGAGGAGGAATCTCGGCATGAACCTCGATCGAAGACGGTAG 240
 Db |||||
 QY 587 TTCCTTACCTTGAACACTATACGATTGSCCCCGAGGTAGATCATCAGATTGTCAAGCTG 646
 Db |||||
 QY 241 TCCCTCTCCTTTGAACACTTACAAAGTTGGTCTGAGCTATACCAAGATCGCCAAAC-- 298
 Db |||||
 QY 647 ATGTAGCTGGTGGTGACGCTCTCTCACGCCGCTCAGTGCAGCTGGGCGTCTTTCACAT 706
 Db |||||
 QY 299 -TGGCGCTGTGGGAGCGCTCCACCCGACCGCCGCAAGGCTGGGCGTCTTTTCAT 357
 Db |||||
 QY 707 TCAGCCCCAAGGCCATGTCTAGAGCTCAAGGATGC 740
 Db |||||
 QY 358 TCACCTCCCAAGGCCCTCTCGGAGCTGAAGACGC 391
 Db |||||

RESULT 14
 B1192498/c
 LOCUS
 DEFINITION
 m4f10fs.f1 Fusarium sporotrichioides Tri 10 overexpressed cDNA library Fusarium sporotrichioides cDNA clone m4f10fs 3', mRNA sequence.

ACCESSION
 B1192498
 VERSION
 B1192498.1 GI:14666177
 KEYWORDS
 EST.
 SOURCE
 Fusarium sporotrichioides
 ORGANISM
 Fusarium sporotrichioides
 Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes; Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
 REFERENCE
 1 (bases 1 to 423)
 Ren,Q., Tag,A., Peplow,A., Lai,H., Kupfer,C., Peterson,A., Beremand M. and Roe,B.
 TITLE
 Analysis of a Fusarium sporotrichioides EST database
 JOURNAL
 Unpublished
 COMMENT
 Other ESTs: m4f10fs.r1
 Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
 Department of Chemistry and Biochemistry
 Advanced Center for Genome Technology, University of Oklahoma
 620 Parrington Oval, Norman, OK 73019, USA
 Tel: 405 325 4912
 Fax: 405 325 7762
 Email: broe@ou.edu
 Contact Dr. Marian Beremand regarding clone availability Included is the best homolog from a blastx search of Genbank nr 04-09-01
 652 3e-68 gi|437882|gb|AAD197 (AF127176)
 trichothecene3-O-acetyltransferase
 Seq primer: M13-20
 High quality sequence stop: 290.

FEATURES
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 /mol_type="mRNA"
 /strain="Tri 10"

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/clone="m4101fs"
/cdb="Fusarium sporotrichioides Tri 10 overexpressed
cdna library"
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript
; 3' end of cDNA cloned into XhoI site of pBlueScript"
BASE COUNT 105 a 121 c 92 g 105 t
ORIGIN
Query Match 18.8%; Score 254.8; DB 12; Length 423;
Best Local Similarity 79.6%; Pred. No. 1.7e-61;
Matches 301; Conservative 0; Mismatches 77; Indels 0; Gaps 0;
QY 979 CTCGGCGCAACAGCATCAGCCTTCGTTTCAGAACTCGACCCCGGAGCATGCGCCAGCGA 1038
Db 423 CTTGGCGCAACAGCATCAGCCTTCGTTTCAGAACTCGACCCCGGAGCATGCGCCAGCGA 364
QY 1039 ACAGAGGTCTCGGAGCTACCTGACACACACCCGACAGTCCACAGTATCCCTGACG 1098
Db 363 ACACAGAGTCTCGGAGCTACCTGACACACACCCGACAGTCCACAGTATCCCTGACG 304
QY 1099 GCTGATGCGGACCATCTACACAGTCTGCTGAGTCTTGGGCCAAGTGGGACTCTGG 1158
Db 303 GCGGATGCGGATCCGTCACAGCATCTGCTGAGTCTTGGGCCAAGTGGGACTCTGG 244
QY 1159 GATTAGGACTTTGGGCTCGGACTTGGGTAAGCCCGAGACTGTGAGACGGCCAACTTTGAG 1218
Db 243 GAGTATGACTTTGGGCTTGGGTAAGCCCGAGACTGTGAGACGGCCAACTTTGAG 184
QY 1219 CTTGTTGAGAGCTTGATGATCTTATCCCAAGAGCTGATGCGGAGTCTGTGGCGG 1278
Db 183 CTTTGTGAGAGTGTGATGATCTTATCCCAAGAGCTGATGCGGAGTCTGTGGCGG 124
QY 1279 CTTTCTGAGGATGAGGATGATGACCGGATGAAGCGGAGTGAAGGATGACCAAGTAT 1338
Db 123 ATTCTCTGAGGATGAGGATGATGAGAGACTAAAGCGGATGAGGATGACCAAGTAC 64
QY 1339 GCGCAGTACGTTGGTTAG 1356
Db 63 GCAAGTATATGGGTAG 46
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RESULT 15
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LOCUS p2e12fs.r1 Fusarium sporotrichioides Tri 10 overexpressed cDNA
DEFINITION library Fusarium sporotrichioides cDNA clone p2e12fs 5', mRNA
sequence.
ACCESSION BI201353
VERSION BI201353.1 GI:14667325
KEYWORDS EST.
SOURCE Fusarium sporotrichioides
ORGANISM Fusarium sporotrichioides
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; mitosporic Hypocreales; Fusarium.
Ren,Q., Tag,A., Peglow,A., Lai,H., Kupfer,C., Peterson,A., Beremand
,M. and Roe,B.
Analysis of a Fusarium sporotrichioides EST database
Unpublished
Contact: Bruce A. Roe, University of Oklahoma, broe@ou.edu
Department of Chemistry and Biochemistry
Advanced Center for Genome Technology, University of Oklahoma
620 Parrington Oval, Norman, OK 73019, USA
Tel: 405 325 4912
Fax: 405 325 7762
Email: broe@ou.edu
Contact Dr. Marian Beremand regarding clone availability Included
is the best homolog from a blastx search of Genbank nr 04-09-01
656 1e-68 gi|4378882|gb|AAD197 (AF127176)
trichothecene3-O-acetyltransfer
Seq primer: T3
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High quality sequence stop: 443.
FEATURES
Location/Qualifiers
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/organism="Fusarium sporotrichioides"
/mol_type="mRNA"
/strain="Tri 10"
/db_xref="taxon:5514"
/clone="p2e12fs"
/cdb="Fusarium sporotrichioides Tri 10 overexpressed
cdna library"
/note="Vector: pBlueScript SK-; Site 1: EcoRI; Site 2:
XhoI; 5' end of cDNA cloned into EcoRI site of pBlueScript
; 3' end of cDNA cloned into XhoI site of pBlueScript"
BASE COUNT 129 a 153 c 104 g 103 t
ORIGIN
Query Match 18.5%; Score 251.2; DB 12; Length 490;
Best Local Similarity 81.1%; Pred. No. 2e-60;
Matches 292; Conservative 0; Mismatches 68; Indels 0; Gaps 0;
QY 3 GGCTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTACCAAGGCTCTTTTCGATCTACAC 62
Db 129 GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACCGCTCTTCTTTCAATCTACAC 188
QY 63 CCAATCAGTCTCTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTTCTCAGCAC 122
Db 189 CCAGATCAGTCTCGTTTACCCCGTCTCTGATCCCTCCAGTATCCCACTATCTCAGCAC 248
QY 123 CTTGAGCAAGGCTTAAAGCGCTTTCGGAAGCGTCCCATGGTGGCAGGCCAGGTCAA 182
Db 249 CCTTGAGGAGGCGCTAAAGCGCTCTCTCAAGCTTCCCATGGTGGCAGGCCAGGTCAA 308
QY 183 AGCCGAGGCGCATTAAGCGAGGGAACACAGGAACTTCCTTTATCGTCCCTTTTGAGGACGT 242
Db 309 GACCGAGGCGCATGAGCGAAGGAACACAGGAACTTCCAGATCATTCATATGAGGAGAC 368
QY 243 TCCTCGTGTGTAGTGAAGACCTTCGCGGATGATTCCTTCAGCGCCACGATCGAGGTAT 302
Db 369 ACCCGGCTTGTGTGAAGACCTTCGCGGATGATTCCTTCAGCGCCACGATCGAGGGGTT 428
QY 303 GAGAAAGCGCGGATACCCCTATGGCGATGTTTGAGGAGAACATCATCGCCCAAGGAAGAC 362
Db 429 GAGAAAGCGCGGTTTCCCTTTAGAGATGTTTGAGGAGAACATCATCGCTCGCGAGGAGAC 488
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Search completed: February 7, 2004, 21:46:40
Job time : 3192 secs

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3	915.6	67.5	12949	14	US-10-074-279-11	Sequence 11, Appl
4	915.6	67.5	13737	14	US-10-074-279-10	Sequence 10, Appl
5	249.8	18.4	1425	14	US-10-074-279-7	Sequence 7, Appli
6	39.2	2.9	1947	12	US-10-369-493-27681	Sequence 27681, A
7	35.8	2.6	2463	12	US-10-320-797-7	Sequence 7, Appli
8	35.4	2.6	2400	12	US-10-369-493-37751	Sequence 37751, A
9	35.2	2.6	837	15	US-10-184-644-352	Sequence 352, App
10	35.2	2.6	837	15	US-10-184-634-352	Sequence 352, App
11	35	2.6	556	13	US-10-063-685-24	Sequence 24, Appl
12	35	2.6	556	15	US-10-184-644-136	Sequence 136, App
13	35	2.6	556	15	US-10-184-634-136	Sequence 136, App
14	34.6	2.6	427	12	US-10-374-780A-932	Sequence 932, App
15	34.6	2.6	1112	13	US-10-027-632-31187	Sequence 31187, A

Qy	121	ACCTTCGAGCAAGGCTCTTAAGCGCTTCTCCGAGCGCTCCCATGGTCCGAGCGCAGGTC	180
Db	121	ACCTTCGAGCAAGGCTCTTAAGCGCTTCTCCGAGCGCTCCCATGGTCCGAGCGCAGGTC	180
Qy	181	AAAGCCGAGGCGCATTTAGCGAGGGAACAACAGAACTTCTTATCGTCCCTTTTGAGGAC	240
Db	181	AAAGCCGAGGCGCATTTAGCGAGGGAACAACAGAACTTCTTATCGTCCCTTTTGAGGAC	240
Qy	241	GTTCCTCGTGTCTAGTGAAGACCTCCGCGATGATCTTCAGCGCCACAGATCGAGGT	300
Db	241	GTTCCTCGTGTCTAGTGAAGACCTCCGCGATGATCTTCAGCGCCACAGATCGAGGT	300
Qy	301	ATGAGAAAGCGGGATACCTATCGGCGATGTTTGACGAGAAATCATATCGCGCAAGGAAG	360
Db	301	ATGAGAAAGCGGGATACCTATGCGGATGTTTGACGAGAAATCATATCGCGCAAGGAAG	360
Qy	361	ACGTTACTATTTGACCTGTGTACTGGTCCGACGACCCAAAGCCTGTATTTCTATTGACG	420
Db	361	ACGTTACTATTTGACCTGTGTACTGGTCCGACGACCCAAAGCCTGTATTTCTATTGACG	420
Qy	421	CTCAACTTCATCAAGGCGGACATCATCTCACATGTCAAACGACAGCAGTGTATTTGAT	480
Db	421	CTCAACTTCATCAAGGCGGACATCATCTCACATGTCAAACGACAGCAGTGTATTTGAT	480
Qy	481	ATGCTAGCGCAAGATGCGGTGATCCGCTTACTCTTCAAGGCGTCCGCTAACGACCATTC	540
Db	481	ATGCTAGCGCAAGATGCGGTGATCCGCTTACTCTTCAAGGCGTCCGCTAACGACCATTC	540
Qy	541	ACCGAAGAGGAATGACGGCCATGAACTCGATCGCAGACGATAGTTCTTACCTTGA	600
Db	541	ACCGAAGAGGAATGACGGCCATGAACTCGATCGCAGACGATAGTTCTTACCTTGA	600
Qy	601	AACCTATAGATTGCGCCCGAGTAGATCATCAGATTCTCAAAGCTGATAGTCTGGTGGT	660
Db	601	AACCTATAGATTGCGCCCGAGTAGATCATCAGATTCTCAAAGCTGATAGTCTGGTGGT	660
Qy	661	GACGTGTTCTCACGCGCGTCAGTGCAGGCTGGCGGTTCTTCAATTCAGCCGCCAGGCC	720
Db	661	GACGTGTTCTCACGCGCGTCAGTGCAGGCTGGCGGTTCTTCAATTCAGCCGCCAGGCC	720
Qy	721	ATGTCAGAGCTCAAGATGCTGTGCTACAGACTCTTGAACGCTCAACAAAGTTCGTGCTG	780
Db	721	ATGTCAGAGCTCAAGATGCTGTGCTACCAAGACTCTTCAAGCATCAACAAAGTTCGTGCTG	780
Qy	781	ACTGACGATGCTCTTTGGCGGCTTCATCTGGAATCGGCGCTCTCGCGTGCCTTCGAAAGA	840
Db	781	ACTGACGATGCTCTTTGGCGGCTTCATCTGGAATCGGCGCTCTCGCGTGCCTTCGAAAGA	840
Qy	841	ATCGATGGCTTCGACCTACCGAGTCTTGCGTGTCTGTTGATGTCGACCGGCAATGGGT	900
Db	841	ATCGATGGCTTCGACCTACCGAGTCTTGCGTGTCTGTTGATGTCGACCGGCAATGGGT	900
Qy	901	GTCTCGAACAACTACCGAGGCTTCTTCAAACATGACCTACCAACTCGCATCGGC	960
Db	901	GTCTCGAACAACTACCGAGGCTTCTTCAAACATGACCTACCAACTCGCATCGGC	960
Qy	961	GAAATCGCAACGAGTCTACCTGGGCAACAGCATCACGCCCTTCGTCAGAACTCGACCCC	1020
Db	961	GAAATCGCAACGAGTCTACCTGGGCAACAGCATCACGCCCTTCGTCAGAACTCGACCCC	1020
Qy	1021	GGGAGCATGCGCCAGCAACAGAGGTCTCGCGAGCTTACGCAACAAACCCGCAAG	1080
Db	1021	GGGAGCATGCGCCAGCAACAGAGGTCTCGCGAGCTTACGCAACAAACCCGCAAG	1080
Qy	1081	TCCACGTAATCCGTGACGGCTGATCGGAGCCCATCTACCGAGTCTAGTCTGCTTGG	1140
Db	1081	TCCACGTAATCCGTGACGGCTGATCGGAGCCCATCTACCGAGTCTAGTCTGCTTGG	1140
Qy	1141	GCCAGGTGGGACTCTGGGATTTACGACTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTG	1200
Db	1141	GCCAGGTGGGACTCTGGGATTTACGACTTTGGGCTCGGACTGGGTAAAGCCCGAGACTGTG	1200
Qy	1201	AGACGCCCAATCTTTGAGCGCTGTGAGAGCTTGTATGTTATGSCCAACAGCCTGAT	1260

```

Db      1201  AGCGGCCAATCTTTGAGCCTGTTGAGAGCTTGAATGTACTTTATGCCAAGAAGCCTGAT 13260
          |||||
Qy      1261  GCGGAGTTCTGTGCGGCGCTTTCTCTGAGGGATGAGGANTGACACCGATTGAAGGCGGAT 13200
          |||||
Db      1261  GCGGAGTTCTGTGCGGCGCTTTCTCTGAGGGATGAGGANTGACACCGATTGAAGGCGGAT 13200
          |||||
Qy      1321  AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
          |||||
Db      1321  AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
          |||||

RESULT 2
US-10-074-279-1
; Sequence 1, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmerson, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic plant and Methods
; FILE REFERENCE: sequence1ist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 1403
; TYPE: DNA
; ORGANISM: Fusarium sporotrichioides
US-10-074-279-1

```

Query Match	67.5%;	Score 915.6;	DB 14;	Length 1403;
Best Local Similarity	80.3%;	Pred. NO. 1.4e-306;		
Mismatches 1097;	Conservative	0;	Mismatches 264;	Indels 3;
Gaps				

483 GGTAGGCAAGATGGGTGATCGCTACTCTCCAGGCGTCCGTACAGCCCATTCAC 542
Db |||||
516 GACAGGCAAGATGCAATATTTCGCTCTCTCCAGGCGTCCGCAACGAATCATTCAC 575
Qy |||||
543 CGAAGAGAAATGACGGCCATCAACCTCGATCGCAAGACGATAGTTCCTTACCTTGA AAA 602
Db |||||
576 CGAGGAGAAATCTCGGCCATGAACTCGATCGCAAGACGATAGTTCCTTCTCTTGA AAA 635
Qy |||||
603 CTATACGATTTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGTGA 662
Db |||||
636 CTACAAAGTTGGTCTGAGCTAGACCAACAGATCGCCAAAC---TGCGCCTGTGGCGA 692
Qy |||||
663 CGCTGTTCTACGGCGGTGAGTCAAGCTGGCGGTCTTTCACATTCAGCCCAAGGCCAT 722
Db |||||
693 CGCTCCACCCGACCGGCAAGCAAGCTGGCGGTCTTTCATTCATCTCCCAAGGCCCT 752
Qy |||||
723 GTCAGAGCTCAAGGATGCTGTACCAAGACTCTTGACGCAATCAACAAAGTTTCGTGTGAC 782
Db |||||
753 CTCGAGCTGAAGACGAGCAACAAAGACTCTTGACGCGTCTGTCGAAGTTTGTCAAC 812
Qy |||||
783 TGACGATGCTTTTCGGGGTTCATCTGGAATCGGCCCTCTCGCGTGTCTCGAAAGAA 842
Db |||||
813 TGATGATGCTTTTCGGGGTTCATCTGGCAATCAACCTCGCGGTGACGCTCGCAAGAT 872
Qy |||||
843 CGATGGCTCTGACCTACCGAGTTCGCGGTGCTGTGATGCTGCAACGGCAATGGGTGT 902
Db |||||
873 GGAATGCTTCCACACTACTGAATTTCTCGCGGTGTGACATGCGGGGCCCAATGGGCGT 932
Qy |||||
903 CTCGAAACAATPACCGAGGCTTCTTCAAAATGACACTTACCAACTCGACCATCGCGGA 962
Db |||||
933 ATCAAGCACATACCCAGGCTTCTTCAAAATGACACTTACCTGACCTGACCGCTGCGGA 992
Qy |||||
963 AATCGCAACGAGTCACTCGCGCAACAGATCAAGCTTCGTTTCAAGAACTCGACCCCGC 1022
Db |||||
993 AATCGCAACGAAACCACTTGGCGCAACAGATCAAGCTCGGCTCGGAACCTCAACAGTGA 1052
Qy |||||
1023 GAGATGCGCCAGGCAACAGAGTCTCGCAAGTACCTGACACAAACCCCGCAAGTC 1082
Db |||||
1053 TCGTTTGGCGAGAGCAACAGAGCTTTGGCGACGCTACATGATGCGCTGCGCTGCAAGTC 1112
Qy |||||
1083 CAACGATPCCCTGACGGCTGATCGGACCCATCTACAGAGCTCATGTGAGTCTTGGGC 1142
Db |||||
1113 GAGGCTCTCCCTGACCGCGGATGGAATCGTCAAGCAGCATCATGTGAGTTCCTGGGC 1172
Qy |||||
1143 CAAGTGGAATCTGGGATACGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG 1202
Db |||||
1173 CAAGTGGAATCTGGGATGATGACTTTGGGTTTGGACTGGGTAAGCCTGAGAGTGTGAG 1232
Qy |||||
1203 ACGGCCAATCTTTGAGCCTGTTGAGAGTTCATGATCTTTATGCCCAGAGCCGTGATGG 1262
Db |||||
1233 AAGACCTCGCTTTGAACTTTGAGAGTTCATGATCTTTATGCCCAGAGCCGTGATGG 1292
Qy |||||
1263 CGAGTCTGTGCGGCGCTTCTCTGAGGATGAGATGATGACCGATTGAAGCGGATAA 1322
Db |||||
1293 GGAGTTTACGGCTGCCATTTCTTGAGGATGAGATGAGAGACTAAGAGCGGATGA 1352
Qy |||||
1323 GGAGTGACCAAGTATGCGAGTACGTTGGTTAG 1356
Db |||||
1353 GGAGTGACCAAGTATGCGCAAGTATATTGGGTAG 1386

RESULT 3

US-10-074-279-11
; Sequence 11, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.

; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 11
; LENGTH: 12949
; TYPE: DNA
; ORGANISM: Plasmid
US-10-074-279-11

Query Match 67.5%; Score 915.6; DB 14; Length 12949;
Best Local Similarity 80.3%; Pred. No. 4.7e-306;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;
Qy 3 GGCTTTCAGATACAGCTGACACCCCTCGGCAGCTACCGGCTCTCTTCGATCTACAC 62
Db 11281 GTCTTTTGACATAGAGCTCGACATCATCGGCAGCAACCGCTCTCTTCTCAATCTACAC 11340
Qy 63 CCAATCAGTCTCTCTACCCGCTCTGTATCTCAATATCCCAATCCCACTATTGTGACAC 122
Db 11341 CCAGTCACTCTCGTTTACCCGCTCTGTATCTCCCTCCAGTATCCCACTCGTACAC 11400
Qy 123 CTTGAGCAAGCTCTTAAGCGCTTCTCGAAGCGCTCCCATGGGTGCGAGGCCAGGTCAA 182
Db 11401 CTTGAGGAGGCTTAAACCGCTCTCTCAACCTTCCCATGGGTGCGGCGCAGGTCAA 11460
Qy 183 AGCCGAGGCAATAGCGAGGGAACAACAGGAACCTTCCTTTATCTGCTCTCTTTGAGGAGCT 242
Db 11461 GACCGAGGCAATAGCGAGGGAACAACAGGAACCTTCCAAAGATCATTCATATGAGGAGAC 11520
Qy 243 TCCTCGTGTGTAGTGAAGACCTCGCGATGATCTTTCAGCGCCGACGATCGAGGGTAT 302
Db 11521 ACCCGGCTTGTGTGAGGAGACCTTCGCTGATGATTCCTCAGCGCAACGATCGAGGGGTT 11580
Qy 303 GAGAAAGCGGGATACCTATGGCGATGTTTGACGAGAAATCATCGGCCCAAGGAAGAC 362
Db 11581 GAGAAAGCGGGTTTCCCTTAGAGATGTTTGACGAGAACTGCTGCTCGAGGAGAC 11640
Qy 363 GTTACCTATTGGACCTGGTACTGGTCCGAGCAACCAAGCCTGTAATTTATTTCAGCT 422
Db 11641 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGGCTGTGTGCTATTTCAGCT 11700
Qy 423 CAACCTTCATCAAGCGGCGACTCATCTCACTGTCAACGCGACGACGCTGCTATGATAT 482
Db 11701 CAACCTTCATTAAGGCGGAGCTCATCTCAGCGTCAACGCGCAACATGGTGTATGGACAT 11760
Qy 483 GGTAGGCAAGATGCGGTGATTCGCTACTCTTCCAGGCGTCCGTAACGACCCATTCAC 542
Db 11761 GACAGGCAAGATGCAATTAATTCGCTCTTCTCCAGGCGTCCGCAACGATCATTCAC 11820
Qy 543 CGAAGAGAAATGACGGCCATGAACCTCGATTCGCAAGACGATAGTTCCTTACCTTGA AAA 602
Db 11821 CGAGGAGAAATCTCGGCCATGAACCTCGATTCGCAAGCGTAGTCTCTCTCTCTG AAAA 11880
Qy 603 CTATACGATTTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGTGTA 662
Db 11881 CTACAAAGTTGGTCTGAGCTAGACCAACCGATCGCCAAACCC---TGCGCTGTGCGGA 11937
Qy 663 CGCTGTTCTCACGCGGCTGAGTCAAGCTGGGCTTCTTCAATTCAGCCCAAGGCCAT 722
Db 11938 CGCTCCACCCGACCGGCAAGGCAAGCTGGGCTTCTTTTCACTCTCCAGAGGCCCT 11997
Qy 723 GTCAGAGCTCAAGATGCTCTTACCAGACTTTGACGCACTCAACAAAGTTTCGTGTGAC 782
Db 11998 CTCGGAGCTCAAGAGCGCAGCCCAAGACTCTTTGACGCGTCTGTCGAAGTTTGTGTCAAC 12057
Qy 783 TGAGATGCTCTTTTCGGCGTTCATCTGGAATTCGGGCTCTCGCGTGTGCTCGAAGAA 842

Db	12058	TGATGATGCTCTTTTGGCGCTTTATTCGGCAATCAACCTCGCGGTFACGTCGCGAAGATT	12117
Qy	843	CGATGCTCTGCACTACCGAGTCTTGCGCGTCTGCTGTGATCTGACCGCAATGGGTGT	902
Db	12118	GGATGCTTCAACACCTPACTGAAATTCGCGCGCTGTGACATGCGGGGCCAATGGGCGT	12177
Qy	903	CTCGAACAACCTACCGAGGCTTCTTTCAAACATGACTTACCAACATCGAACCATCGCGGA	962
Db	12178	ATCAAGCACATACCGAGGCTTCTTTCAAACATGACTTACCAACATCGAACCATCGCGGA	12237
Qy	963	AATGGCAAGGAGTCACTCGGGCGCAACAGCATCAGCCCTTGTTTCAAGAACTCGACCCGCG	1022
Db	12238	AATCGCAACGAACCACTTTGGCGCAACAGCATCAGCCCTGCGCTCGGAACCTCAACAGTGA	12297
Qy	1023	GAGCATGCGCCAGCGAACAAGAGTCTCTCGGAGCTACCTGCAACAACACCCCGCAAGTC	1082
Db	12298	TCGTTTGGCAGACGAACAACAGCTTTTGGCGAGTACATGCTGCGCTTGCCTGCAAGTC	12357
Qy	1083	CAACGTATCCCTGACCGGCTGATGCGGACCACTTACCAGCGTCATGCTGAGTCTTTGGGC	1142
Db	12358	GAGGCTCTCCCTGACCGCGGATCGGAATCCGTCGAAGCAGCATCATGCTGAGTCTCTGGGC	12417
Qy	1143	CAAGGTGGAGCTCTGGGAATTAAGACTTTTGGGCTCGGACATGGGTGAAGCCCGAGACTGTGAG	1202
Db	12418	CAAGGTGGGATGCTGGGAGTATGACTTTTGGGTTTGGACTGGGTAAAGCCCTGAGTGTGAG	12477
Qy	1203	ACGGCCAACTTTTGACCTGTTGAGAGCTTTGATGTACTTTATGCCCCAAGAAGCCGTGATGG	1262
Db	12478	AAAGACCTCGCTTTGAACCTTTTGGAGAGTTTGAATGTACTTTATGCCCAAGAAGCCGTGATGG	12537
Qy	1263	CGAGTTCTGTGCGGCGCTTTCTCTGAGGGATGAGGATATGGACCGATTTGAAGCGCGAATAA	1322
Db	12538	GGAGTTTACGGCGTCACTTCTCTGAGGAGTGAAGGATATGGAGAGACTAAAGCGCGATGA	12597
Qy	1323	GGAGTGACCAAGTATGCGCAGTACGTTGGTTAG	1356
Db	12598	GGACTGCAAAAGTACGAAAGTATATTTGGGTAG	12631

RESULT 4

```

US-10-074-279-10
; Sequence 10, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence1st
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence:Plasmid
US-10-074-279-10

Query Match          67.5%;   Score 915.6;   DB 14;   Length 13737;
Best Local Similarity 80.3%;   Pred. No. 4.9e-306;
Matches 1087;   Conservative 0;   Mismatches 264;   Indels 3;   Gaps 1;

3  GGCTTTTCAAGATACAGCTCGACACCCCTCGGCCAGCTACCAAGGCCTCCTTTGCATCTTAC 62

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QY 1143 CAAGTGGGACTCTGGGATTAGGACTTTGGGCTCGACTGGTAAAGCCCGAGACTGTGAG 1202
Db |||||
QY 1187 CAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGAGTGGGTAAAGCCCTGAGAGTGTGAG 1246
Db |||||
QY 1203 ACGGCCAATCTTTGAGCCCTGTTGAGAGCTTGATGTAATTTATGCCCAAGAGCCCTGATGG 1262
Db |||||
QY 1247 AAGACCTCGCTTTGAACCTTTGAGAGTTGATGTAATTTATGCCCAAGAGCCCTGATGG 1306
Db |||||
QY 1263 CGAGTTCTGTCGGGCGCTTTCTCTGAGGGATGAGGATATGAGCCGATTAAGAGCGGATAA 1322
Db |||||
QY 1307 GGAGTTTACGGCGCTCCATTTCTCTGAGGATGAGGATATGAGAGACTAAAGGGGATGA 1366
Db |||||
QY 1323 GGAGTGGACCAAGTATGCGAGTACGTTGGTTAG 1356
Db |||||
QY 1367 GGAGTGGACAAAGTACGCAAGTATATTGGGTAG 1400
Db |||||
RESULT 5
US-10-074-279-7
; Sequence 7, Application US/10074279
; Publication No. US20020162136A1
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequence list
; CURRENT APPLICATION NUMBER: US/10/074,279
; CURRENT FILING DATE: 2002-02-12
; PRIOR APPLICATION NUMBER: US/09/538,414
; PRIOR FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-10-074-279-7
Query Match 18.4%; Score 249.8; DB 14; Length 1425;
Best Local Similarity 51.9%; Pred. No. 2.4e-75;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;
QY 16 CAGCTCGACACCCCTCGGCCAGCTACCGGCTCTCTTCGATCTACACCAATCAGTCTC 75
Db |||||
QY 64 CAATTTGATATTTTGGGACAAACCTTCGCTATACAACTATACACTCAATATGCTCT 123
Db |||||
QY 76 CTCTACCCCGTCTCTGATTCCTCTCAATATCCCACTATTTGTGAGCACCCTTCGAGCAAGGT 135
Db |||||
QY 124 ATCTACCGTGTAACAGATCTCTCTGCTCATGACCATATCGTAATACCTTAAACAGGA 183
Db |||||
QY 136 CTTAAGCGCTTCTCGAAGCGCTGCGATGGTTCGAGCCAGGTCGAAGCCGAGGCAT 195
Db |||||
QY 184 CTTGAAACATTTGGGTAAATTTCCAGTGGCTAGCAGGAAATGCTGTAATGCAAGGTGCT 243
Db |||||
QY 196 AGCGAGGGAACACAGGAATCTCTTTATCTGCTTTTGGAGGAGTTCCTCGTGTGTA 255
Db |||||
QY 244 GACGAGGTAACTGGGTACCTTACAGAAATTTGCCGTGAGCAAAATTCAC---TTATC 300
Db |||||
QY 256 GTGAAAGACCTCCGCGATGATCTCTTCAGCGCCACGATCGAGGGTATGAGAAAGCGGGA 315
Db |||||
QY 301 GTCCAAGATCTTCGAGAGATCTGTCTGCCCCCAACATGATTCGCTTGAAGAAAGCTGAC 360
Db |||||
QY 316 TACCTATGGGATGTTTGAAGAGAACATATCGCGCCAAAGAGACGTT-----ACCT 369
Db |||||
QY 361 TTTCTATCTACATGTTAGACGAAAGACTTTTGGGCTTTCATGACTATCAATCCACCT 420
Db |||||
QY 370 ATTGGACCTGCTAGTGGTCCCGACGACCAAGCCTGTAATCTTATTTGACGCTCACTTC 429
Db |||||

RESULT 6

US-10-369-493-27681/c

; Sequence 27681, Application US/10369493

; Publication No. US20030233675A1

; GENERAL INFORMATION:

Db |||||
QY 421 GGAACACTATAGGTATGGCCGCCAAGAGTGGGCTGTATTTGCAAGTCAACCAACTTT 480
QY |||||
QY 430 ATCAAGGGCGGACTCATCTCTCAACGACAGACGCGTGTATGATGATGTAGGC 489
Db |||||
QY 481 ATCTCCGGCGGCTCGTCTTAACCTATTTGCGGCGAGCACAATATTTATGATATACAGGA 540
Db |||||
QY 490 CAAGATGCGGTGATCCGCTACTCTCCAAGGGGTGCGGTAAAGCCATTCACCGAAGAG 549
Db |||||
QY 541 CAGGAAGATATCATCAACTGCTCAATAAATCTTGCCACCAAAACCTTTCTCTGATGAA 600
Db |||||
QY 550 GAATGACGGCCATCAACCTCGATCGCAGAGAGTAGTTCTCTTACCTTGAACATATAGC 609
Db |||||
QY 601 GAATGCTCATTTGGAATATATAGATAAAGCAAACTATTCTCTTTGTTGATGAACACTTGG 660
Db |||||
QY 610 ATT---GGCCCCGAGGTAGATCATCAAGTCTCAAAAGCTGATGCTGGTGGTGCACGCT 666
Db |||||
QY 661 GAACCCGACACACGCTAGTTTCATGAATAGTGGAAACCTCTAGAAATACAAGTGGAGAG 720
Db |||||
QY 667 GTTCTCAGCGCGTCACT-----GCAAGCTGGGCGTCTTCAATTCAGCCCCAAG 717
Db |||||
QY 721 GAAAAGGAACAGTCTTGTCTTCGAACTCTACTTTGGGCTTATGTTGAATTTTCTGCTATC 780
Db |||||
QY 718 GCCATGTCAGAGCTCAAGGATGCTGTACCAAGACTCTTTGACGATCAACAAGTCTGTG 777
Db |||||
QY 781 TCATTGCAATCTGAGGATTTGGCAATGACAGATGATCTCTGCGCACAAATTTGTC 840
Db |||||
QY 778 TCGACTGACGATGCTCTTTTCGGCGTTCATCTGGAATCGGCTCTCGCGTGGCTCGAA 837
Db |||||
QY 841 TCCACTGATGATATCGTCACTGCTTTTCATCTGGAATCAGTTTCTCGAGCCCGTTATCT 900
Db |||||
QY 838 AGAATCGATGCTCTGACCTTACCGAGTCTTCCGCTGCTGTGTGATGCTGCGACCGCAATG 897
Db |||||
QY 901 CGACTTAAACCAAGAAACGAAATCAAATTTAGGCGCTGCTGTGGATGTTAGAAAACGGCTA 960
Db |||||
QY 898 GGTCTCTGAAACAACTACCGAGGCTCTTTCAAACATGACCTTACCACCACTCGACCATC 957
Db |||||
QY 961 GGACTCCCCGAAACGATATCCAGGGTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020
Db |||||
QY 958 GCGAAATCGCCAAACGAGTCACTCGGCGCAACAGCATCACGCTTCGTTTCAGAACTCGAC 1017
Db |||||
QY 1021 AABAGCTTGGATCATATAAAGTTTGGGCTTCTTGATCAGATTCGCAAGAGTAGAC 1080
Db |||||
QY 1018 CCCCGAGCA-----TGCGCCAGCAACAAGAGTCTTCGCGAGTACTTCGACCAACAC 1071
Db |||||
QY 1081 CCTAAGTCTTCGATTTGGCCCTATAATACATGCGACCTTGCTAGCTCTCTTTAGCCGATGC 1140
Db |||||
QY 1072 CCCGACAGTCCAAAGTATCCCTGACGGCTGATGGGACCCATCTACAGCGTATGCTG 1131
Db |||||
QY 1141 CCGGACAGACTAAGGTTTCTATACCTCAACCAATGATATCTTTATCTGGAATTTATGCTC 1200
Db |||||
QY 1132 AGTTCTTTGGGCAAGGTGGGACTCTGGGATTAACGACTTTGGGCTCGGACTGGGTAAGCCC 1191
Db |||||
QY 1201 AGTTCTGGGCAAAAGTCAGCTCTATGACGTTGATTTCAATCTAGGGCTTGGAGAGCCC 1260
Db |||||
QY 1192 GAGACTGTGAGACGGCAATCTTTGAGCTGTTGAGAGCTTGTATGATCTTTATGCCCAAG 1251
Db |||||
QY 1261 AAGAGTGTATACGCGCGCGCTTCATTTCCCTTGAGAGCCCTAATATATTTTATGCTAGA 1320
Db |||||
QY 1252 AAGCTGATGCGAGTCTGTGCGGCGCTTCTCTGAGGAGTATGAGATATGACCGGATTG 1311
Db |||||
QY 1321 TCCTCCAGAGGTGAAATGGTGGTTGCTCTTTGCTTTAGATAAAGATTTGGAGTGGCTG 1380
Db |||||
QY 1312 AAGCGGATAAGAGTGGACCAAGTATGC 1340
Db |||||
QY 1381 AATCGGATAAGATGACAAATATATGC 1409
Db |||||

```

; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 27681
; LENGTH: 1947
; TYPE: DNA
; ORGANISM: Neurospora crassa
US-10-369-493-27681

Query Match      2.9%; Score 39.2; DB 12; Length 1947;
Best Local Similarity 53.2%; Pred. No. 0.038;
Matches 83; Conservative 0; Mismatches 73; Indels 0; Gaps 0;

QY 1050 CGGAGCTACTGTCACAAACCCCGCAAGTCCACGTATCCCTGACGGCTGATCGGA 1109
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1854 CCCGACATAGTGTGCGCACACCAGTGCATGACAAACGTGTAATGGCGCGCTGTGGCGG 1795

QY 1110 CCATCTACAGGCTGATGCTGAGTTCTTGGGCCAAGTGGGACTCTGGGATTAACACTT 1169
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1794 CGCTGGAATCGCGCTTCACTGTTTTCATGTCGGAACGTGCGGCTCTTGCCTCCGACTC 1735

QY 1170 TGGGCTCGGACTGGTAAGCCCGAGACTGTGAGACG 1205
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1734 GTAAATGGGCTGTCAAAGCTGACAAAGGTGAAGG 1699

RESULT 7
US-10-320-797-7/c
; Sequence 7, Application US/10320797
; Publication No. US20040014955A1
; GENERAL INFORMATION:
; APPLICANT: Eroshkin, Alexey M.
; APPLICANT: Zamudio, Carlos
; TITLE OF INVENTION: IDENTIFICATION OF ESSENTIAL GENES OF CRYPTOCOCCUS NEOFORMANS AND
; TITLE OF INVENTION: METHODS OF USE
; FILE REFERENCE: 10182-021-999
; CURRENT APPLICATION NUMBER: US/10/320,797
; CURRENT FILING DATE: 2002-12-16
; PRIOR APPLICATION NUMBER: 60/341,261
; PRIOR FILING DATE: 2001-12-17
; NUMBER OF SEQ ID NOS: 3361
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 7
; LENGTH: 2463
; TYPE: DNA
; ORGANISM: Cryptococcus neoformans
US-10-320-797-7

Query Match      2.6%; Score 35.8; DB 12; Length 2463;
Best Local Similarity 53.1%; Pred. No. 0.66;
Matches 76; Conservative 0; Mismatches 67; Indels 0; Gaps 0;

QY 2 TGGCTTTCAAGATACAGTGCACACCTCGCCAGCTACAGGCTCTTTCGATCTACA 61
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2371 TGGGTTTCAAAAATGGGTGCTTGAGCTCGCCAAAGCAGAAAAGAACTCGGGCTTTCT 2312

QY 62 CCCAAATCAGTCTCTCTACCCCGTCTCTGATCTCTCAATATCCCACTATTTCAGCA 121
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2311 TCGACGTCGTATCGTCTGCTCCGTCACTGTTCTTCTCAGCGCGTACCGTCTCGTG 2252

QY 122 CTTTCGAGCAAGGCTTTAAGCGC 144
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2251 CCGTTGCAGAGGAAGGAAGGCGC 2229
```

RESULT 8

```

US-10-369-493-37751
; Sequence 37751, Application US/10369493
; Publication No. US20030233675A1
; GENERAL INFORMATION:
; APPLICANT: Cao, Yongwei
; APPLICANT: Hinkle, Gregory J.
; APPLICANT: Slater, Steven C.
; APPLICANT: Goldman, Barry S.
; APPLICANT: Chen, Xianfeng
; TITLE OF INVENTION: EXPRESSION OF MICROBIAL PROTEINS IN PLANTS FOR PRODUCTION OF
; TITLE OF INVENTION: PLANTS WITH IMPROVED PROPERTIES
; FILE REFERENCE: 38-10(52052)B
; CURRENT APPLICATION NUMBER: US/10/369,493
; CURRENT FILING DATE: 2003-02-28
; PRIOR APPLICATION NUMBER: US 60/360,039
; PRIOR FILING DATE: 2002-02-21
; NUMBER OF SEQ ID NOS: 47374
; SEQ ID NO 37751
; LENGTH: 2400
; TYPE: DNA
; ORGANISM: Pseudomonas fluorescens
US-10-369-493-37751
```

```

Query Match      2.6%; Score 35.4; DB 12; Length 2400;
Best Local Similarity 56.4%; Pred. No. 0.89;
Matches 66; Conservative 0; Mismatches 51; Indels 0; Gaps 0;

QY 487 GGCCAAAGATCGGTGATCCGTCTACTCTCAAGCGTGCCTAAGCCATCCATTCACCGAA 546
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1375 GGCTGTGCTGCGCTGGACCTGGCGACCGGCAAGTGGCTGGAATCACTACCACTTCCACCAC 1434

QY 547 GAGGAATGACGGCCATGACCTGATCGCAAGCATAGTCTCTTACCTTGAAAC 603
      ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 1435 CACGACCTGTGGACATGGACGTGGCGACGCCCAACCCCTGCTGGHACNTGAAACC 1491
```

RESULT 9

```

US-10-184-644-352/c
; Sequence 352, Application US/10184644
; Publication No. US20030044930A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Deenoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C227
; CURRENT APPLICATION NUMBER: US/10/184,644
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-644-352
```

```

Query Match      2.6%; Score 35.2; DB 15; Length 837;
Best Local Similarity 12.6%; Pred. No. 0.6;
Matches 52; Conservative 120; Mismatches 242; Indels 0; Gaps 0;

QY 835 GAAAGATCGATGGCTCTGCACCTACCGAGTTCTCCGCTGCTGTGTGATGCTCGACCGCA 894
```

Db 675 GWH.MMSC..YHGCTD.GYC.BGSSSH.SG.ACHBY...BRRC.TYT.GA.MG.H. 616
Qy 895 ATGGTGTCTGACAACTACCCAGCGCTTCTTCAAAACATGACCTACCAACTCGACC 954
Db 615 .TBCARY.BWHK.C..SM..HAYDNRTG...Y.A.TSCA.GH.ANGSY.YAYYC.GRMC 556
Qy 955 ATCGCGAAATCGCAACGAGTCACTCGCGCAACAGCATACGCGCTTGGTTCAGAACTC 1014
Db 555 CNY.B.YAGHYSS..BCCGAYSGHW.CW.CWCCT...N.H...HKD.GYCKGT.T.C 496
Qy 1015 GACCCGCGAGCATCGCGCAGCAAGAGGCTCTCGCGAGCTTCTGCAACAAACCC 1074
Db 495 G.ACHTW.SDMA.GKTDEN.DCSGW.TTG.....GDYSH.C.A..G.YHTRHMC..AB 436
Qy 1075 GACAGTCAAGCATCTCTGAGCGCTGATCGGACCATCTACAGCGTCTGATGAGT 1134
Db 435 .D..T..MH..GDCRCH..HA..YTS.G.SW....HBDTKB.TKBDYSAS..CN.S.G. 376
Qy 1135 TCTTGGCGAAGTGGGACTCTGGGATTACGACTTGGGCTCGGACTGGTAAGCCCGAG 1194
Db 375 MSNHD.KN.BDC..DTTA.TS..CHH.B.TGSYT.HGBACBHTKC.AHGASBCG.H.YA. 316
Qy 1195 ACTGTGAGCGCAATCTTTGAGCGCTTGTGAGAGCTTGATGCTACTTTATGCC 1248
Db 315 ..TAH.DH.CSH..AN.CY.WTG.SY.A.TTS.CB..C..CSC..B.YABB.SB 262

RESULT 10

US-10-184-634-352/c
; Sequence 352, Application US/10184634
; Publication No. US200300686441
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/184,634
; CURRENT FILING DATE: 2002-06-28
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 352
; LENGTH: 837
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-184-634-352

Query Match 2.6%; Score 35.2; DB 15; Length 837;
Best Local Similarity 12.6%; Pred. No. 0.6;
Matches 52; Conservative 120; Mismatches 242; Indels 0; Gaps 0;
Qy 835 GAAAGATGATGCTCTGCACTACCGAGTCTTCTGCGGTGCTGATGCTCGCGCA 894
Db 675 GWH.MMSC..YHGCTD.GYC.BGSSSH.SG.ACHBY...BRRC.TYT.GA.MG.H. 616
Qy 895 ATGGTGTCTGACAACTACCCAGCGCTTCTTCAAAACATGACCTACCAACTCGACC 954
Db 615 .TBCARY.BWHK.C..SM..HAYDNRTG...Y.A.TSCA.GH.ANGSY.YAYYC.GRMC 556
Qy 955 ATCGCGAAATCGCAACGAGTCACTCGCGCAACAGCATACGCGCTTGGTTCAGAACTC 1014
Db 555 CNY.B.YAGHYSS..BCCGAYSGHW.CW.CWCCT...N.H...HKD.GYCKGT.T.C 496

Qy 1015 GACCCGCGAGCATCGCGCAGCAAGAGGTTCTCGGAGCTACTCTGCAACAAACCC 1074
Db 495 G.ACHTW.SDMA.GKTDEN.DCSGW.TTG.....GDYSH.C.A..G.YHTRHMC..AB 436
Qy 1075 GACAGTCAAGCATCTCTGAGCGCTGATCGGACCATCTACAGCGTCTGATGAGT 1134
Db 435 .D..T..MH..GDCRCH..HA..YTS.G.SW....HBDTKB.TKBDYSAS..CN.S.G. 376
Qy 1135 TCTTGGCGAAGTGGGACTCTGGGATTACGACTTGGGCTCGGACTGGTAAGCCCGAG 1194
Db 375 MSNHD.KN.BDC..DTTA.TS..CHH.B.TGSYT.HGBACBHTKC.AHGASBCG.H.YA. 316
Qy 1195 ACTGTGAGCGCAATCTTTGAGCGCTTGTGAGAGCTTGATGCTACTTTATGCC 1248
Db 315 ..TAH.DH.CSH..AN.CY.WTG.SY.A.TTS.CB..C..CSC..B.YABB.SB 262

RESULT 11

US-10-063-685-24/c
; Sequence 24, Application US/10063685
; Publication No. US20030180909A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; CURRENT APPLICATION NUMBER: US/10/063,685
; CURRENT FILING DATE: 2002-05-08
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 24
; LENGTH: 556
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-063-685-24

Query Match 2.6%; Score 35; DB 13; Length 556;
Best Local Similarity 7.4%; Pred. No. 0.56;
Matches 33; Conservative 142; Mismatches 268; Indels 0; Gaps 0;
Qy 525 CCGTAACGACCCATTACCGAGAGGAATGACGCCATGAACTCGATCGCAAGCAT 584
Db 509 S.G..R.GCSCSC.CSS.HS.H..HBHNCNRTNNKMSAKBY.TK.Y....H.MSAHB.B 450
Qy 585 AGTTCTTACCTTGAAACTATACGATTGGCCCGAGGTAGATCATCAGATTGTCAAGC 644
Db 449 .NNC.NT.CNCAET..RYSWCMCNWGH.NCNETTKY.HNGENS..SSW.MMT.M.M.M 390
Qy 645 TGATGTAGCTGGTGGTGACGCTGTTCACGCGGTCAGTGCAAGCTGGGGTCTTCAC 704
Db 389 BHAB.YH.SACTAA.Y...DD.Y.YTS.TS.S.SYS.YCT...M..CGC..BM.SB.BS 330
Qy 705 ATTACGCCCCAAGCCATGTCAGAGTCAAGGATGCTGTACCAAGACTCTTGACGATC 764
Db 329 NH.KNK.THS.MBH..HKBS..N..C.Y.TBK.KTH..NNW..H.HC.NT.GCYK.NSG 270
Qy 765 AACAAATGCTGCTGACTGACGATGCTCTTTCGCGCTTCTGCGAATCGGCTCTCG 824
Db 269 RNRG.MBAB..CYGDSGR.KM..TDAG.TA.NBBSBMSBHCTBT..C.T.AYTBT.TYAB. 210
Qy 825 CGTGCTCTCGAAGAACTGATGCTCTGACCTACCGAGTCTTCTGCGTCTGTGTGATG 884
Db 209 .M.MY.BHC..M..ARMSBG..R.HA.DR.SNB.Y.KY...YTW.HN.K...NBNCBB 150
Qy 885 TCGACCGGCAATGGGTGCTCTCGAACAACCTACCGAGGCTTCTTCAAAACATGACCTACCA 944

Db 149 RYM..B..HM...SN.KR.DCRAMB.KHN.SM.TN...M...H.MMRYST.BT..DNG. 90

Qy 945 CAACTCGACCATCGGCGAATCG 967

Db 89 .SBBSM.HHMS..SRM..K..SG 67

RESULT 12

US-10-184-644-136/c

; Sequence 136, Application US/10184644

; Publication No. US2003004930A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC227

; CURRENT FILING DATE: 2002-06-28

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 136

; LENGTH: 556

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-644-136

Query Match 2.6%; Score 35; DB 15; Length 556;

Best Local Similarity 7.4%; Pred. No. 0.56;

Matches 33; Conservative 142; Mismatches 268; Indels 0; Gaps 0;

Qy 525 CGGTAAAGCCATTCACCAAGAGAAATGACGGCCATCAACCTCGATCGAAGCAT 584

Db 509 S.G..R.GCSCC.CSS.HS.H..HBHNCNRTNKMVSAKEY.TK.Y....H.MSAHB.B 450

Qy 585 AGTTCTTACTTGAAACTATACGATGGCCCGGAGGTAGATCATCAGATTGTCAAAGC 644

Db 449 .NNC.NT.CNCABT..RYSMCMNWGHH.NCCTTKY.HNGNS..SSW.MMT.M.M.M 390

Qy 645 TGATGTAGTGGTGGTGAACGCTGTTCTACGCGCGTCAAGTCAAGTGGGGTCTTCAC 704

Db 389 BHAB.YH.SACTTAA.Y...DD.Y.YTS.TS.S.SYS.YCT...M..CGC..BM.SB.BS 330

Qy 705 ATTCAGCCCCAAGCCATGTCAGAGTCAAGGATGCTGCTACCAAGACTCTTGACGATC 764

Db 329 NH.KNK.THS.MBH..HKBS..N..C..Y.TBK.KTH..NNW..H.HC.NT.GCYK.NSG 270

Qy 765 AACAAAGTGTGTCGACTGACGATGCTTTTCGGCTTCATCTGGAATCGGCTCTCG 824

Db 269 RNRG.MBAB.CYDGR.KM..TDAG.TA.NBBSBMSBHCTBT.C.T.AYTTB.TYAB. 210

Qy 825 CGTGGCTGTGTCGACTGACGATGCTTTTCGGCTTCATCTGGAATCGGCTCTCG 884

Db 209 .M.MY.BHC..M..ARMSBG..R.HA.DR.SNB.Y.KY...YTW.HN.K..NENCBHR 150

Qy 885 TCGACCGCAATGGGTGTCGAAACAATACCCAGGCTTCTTCAAAACATGACCTACCA 944

Db 149 RYM..B..HM...SN.KR.DCRAMB.KHN.SM.TN...M...H.MMRYST.BT..DNG. 90

Qy 945 CAACTCGACCATCGGCGAATCG 967

Db 89 .SBBSM.HHMS..SRM..K..SG 67

RESULT 14

US-10-374-780A-932

; Sequence 932, Application US/10374780A

; Publication No. US2004001927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

RESULT 13

US-10-184-634-136/c

; Sequence 136, Application US/10184634

; Publication No. US2003006884A1

; GENERAL INFORMATION:

; APPLICANT: Baker, Kevin P.

; APPLICANT: Chen, Jian

; APPLICANT: Desnoyers, Luc

; APPLICANT: Goddard, Audrey

; APPLICANT: Godowski, Paul J.

; APPLICANT: Gurney, Austin L.

; APPLICANT: Pan, James

; APPLICANT: Smith, Victoria

; APPLICANT: Watanabe, Colin K.

; APPLICANT: Wood, William I.

; APPLICANT: Zhang, Zemin

; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC

; TITLE OF INVENTION: ACIDS ENCODING THE SAME

; FILE REFERENCE: P3430RIC217

; CURRENT FILING DATE: 2002-06-28

; Prior Application removed - See File Wrapper or Palm

; NUMBER OF SEQ ID NOS: 612

; SEQ ID NO 136

; LENGTH: 556

; TYPE: PRT

; ORGANISM: Homo Sapien

US-10-184-634-136

Query Match 2.6%; Score 35; DB 15; Length 556;

Best Local Similarity 7.4%; Pred. No. 0.56;

Matches 33; Conservative 142; Mismatches 268; Indels 0; Gaps 0;

Qy 525 CGGTAAAGCCATTCACCAAGAGAAATGACGGCCATCAACCTCGATCGAAGCAT 584

Db 509 S.G..R.GCSCC.CSS.HS.H..HBHNCNRTNKMVSAKEY.TK.Y....H.MSAHB.B 450

Qy 585 AGTTCTTACTTGAAACTATACGATGGCCCGGAGGTAGATCATCAGATTGTCAAAGC 644

Db 449 .NNC.NT.CNCABT..RYSMCMNWGHH.NCCTTKY.HNGNS..SSW.MMT.M.M.M 390

Qy 645 TGATGTAGTGGTGGTGAACGCTGTTCTACGCGCGTCAAGTCAAGTGGGGTCTTCAC 704

Db 389 BHAB.YH.SACTTAA.Y...DD.Y.YTS.TS.S.SYS.YCT...M..CGC..BM.SB.BS 330

Qy 705 ATTCAGCCCCAAGCCATGTCAGAGTCAAGGATGCTGCTACCAAGACTCTTGACGATC 764

Db 329 NH.KNK.THS.MBH..HKBS..N..C..Y.TBK.KTH..NNW..H.HC.NT.GCYK.NSG 270

Qy 765 AACAAAGTGTGTCGACTGACGATGCTTTTCGGCTTCATCTGGAATCGGCTCTCG 824

Db 269 RNRG.MBAB.CYDGR.KM..TDAG.TA.NBBSBMSBHCTBT.C.T.AYTTB.TYAB. 210

Qy 825 CGTGGCTGTGTCGACTGACGATGCTTTTCGGCTTCATCTGGAATCGGCTCTCG 884

Db 209 .M.MY.BHC..M..ARMSBG..R.HA.DR.SNB.Y.KY...YTW.HN.K..NENCBHR 150

Qy 885 TCGACCGCAATGGGTGTCGAAACAATACCCAGGCTTCTTCAAAACATGACCTACCA 944

Db 149 RYM..B..HM...SN.KR.DCRAMB.KHN.SM.TN...M...H.MMRYST.BT..DNG. 90

Qy 945 CAACTCGACCATCGGCGAATCG 967

Db 89 .SBBSM.HHMS..SRM..K..SG 67

RESULT 14

US-10-374-780A-932

; Sequence 932, Application US/10374780A

; Publication No. US2004001927A1

; GENERAL INFORMATION:

; APPLICANT: Sherman, Bradley K

```
; APPLICANT: Riechmann, Jose Luis
; APPLICANT: Jiang, Cai-Zhong
; APPLICANT: Heard, Jacqueline E
; APPLICANT: Haake, Volker
; APPLICANT: Creelman, Robert A
; APPLICANT: Ratcliffe, Oliver
; APPLICANT: Adam, Luc J
; APPLICANT: Reuber, T. Lynne
; APPLICANT: Keddle, James
; APPLICANT: Broun, Pierre E
; APPLICANT: Pilgrim, Marsha L
; APPLICANT: Dubell III, Arnold T
; APPLICANT: Pineda, Onaira
; APPLICANT: Yu, Guo-Liang
; TITLE OF INVENTION: POLYNUCLEOTIDES AND POLYPEPTIDES IN PLANTS
; FILE REFERENCE: MBI-0047 CIP
; CURRENT APPLICATION NUMBER: US/10/374,780A
; CURRENT FILING DATE: 2003-02-25
; PRIOR APPLICATION NUMBER: 09/837,944
; PRIOR FILING DATE: 2001-04-18
; PRIOR APPLICATION NUMBER: 60/310,847
; PRIOR FILING DATE: 2001-08-09
; PRIOR APPLICATION NUMBER: 09/934,455
; PRIOR FILING DATE: 2001-08-22
; PRIOR APPLICATION NUMBER: 60/336,049
; PRIOR FILING DATE: 2001-11-19
; PRIOR APPLICATION NUMBER: 60/338,692
; PRIOR FILING DATE: 2001-12-11
; PRIOR APPLICATION NUMBER: 10/171,468
; PRIOR FILING DATE: 2002-06-14
; PRIOR APPLICATION NUMBER: 10/225,066
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,067
; PRIOR FILING DATE: 2002-08-09
; PRIOR APPLICATION NUMBER: 10/225,068
; PRIOR FILING DATE: 2002-08-09
; NUMBER OF SEQ ID NOS: 2906
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 932
; LENGTH: 427
; TYPE: DNA
; ORGANISM: Zea mays
; FEATURE:
; OTHER INFORMATION: Predicted polypeptide sequence is orthologous to G568
US-10-374-780A-932

Query Match          2.6%; Score 34.6; DB 12; Length 427;
Best Local Similarity 50.3%; Pred. No. 0.67;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 11 AGATACAGCTCGACACCTCGGCAGCTACCGAGCCTCCTTTCGATCTTACCAATCA 70
Db 2 AAAAAATGCACACAGCAGCAAGTCCAAACCAATATTCCTTCGATCTTAACTTGTACT 61
QY 71 GTCTCTCTACCCGCTCTCTGATTCCTCAATATCCCACTATTGTTCAGCACCTTCGAGC 130
Db 62 GCTACTGCTACCAACCAATATTAATCTATATATTTCAATTCCTTCGCCCCCTTCAGAA 121
QY 131 AAGTCTTAAGCGCTTCTCCGAAGCCGCTCCCATGGTGCAGGCGCAGGT 179
Db 122 TTGGGTGGATGAGGTTCTCCGAAGTGAGCTCTTGTTGGGAGGACCACT 170
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```
RESULT 15
US-10-027-632-31187
; Sequence 31187, Application US/10027632
; Publication No. US20030204075A9
; GENERAL INFORMATION:
; APPLICANT: Wang, David G.
; TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
; POLYMORPHISMS IN THE HUMAN GENOME
; FILE REFERENCE: 108827.129
; CURRENT APPLICATION NUMBER: US/10/027,632
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; CURRENT FILING DATE: 2002-04-30
; PRIOR APPLICATION NUMBER: US 60/218,006
; PRIOR FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 60/198,676
; PRIOR FILING DATE: 2000-04-20
; PRIOR APPLICATION NUMBER: US 60/193,483
; PRIOR FILING DATE: 2000-03-29
; PRIOR APPLICATION NUMBER: US 60/185,218
; PRIOR FILING DATE: 2000-02-24
; PRIOR APPLICATION NUMBER: US 60/167,363
; PRIOR FILING DATE: 1999-11-23
; PRIOR APPLICATION NUMBER: US 60/156,358
; PRIOR FILING DATE: 1999-09-28
; PRIOR APPLICATION NUMBER: US 60/146,002
; PRIOR FILING DATE: 1999-08-09
; NUMBER OF SEQ ID NOS: 325720
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 31187
; LENGTH: 1112
; TYPE: DNA
; ORGANISM: Human
US-10-027-632-31187

Query Match          2.6%; Score 34.6; DB 13; Length 1112;
Best Local Similarity 51.6%; Pred. No. 1.1;
Matches 79; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 941 ACCAACTCGACCATCGCGGAAATCGCAACGAGTCACTCGCGCAACAGCATCACGCC 1000
Db 867 ATCACACCTGATCTACTGAGCACTCAATTCCTCTCACTAGACCCACAGCCAGTGCC 926
QY 1001 TTGTTTCAGAACTCGACCCCGGAGCATGCGCCAGCGAACAAGAGTTCGCGACGTACC 1060
Db 927 GGAGTTATCGCGTGGAAACCTCGGACCCACAGCCAGTTCGCGAGTTCGCGTGAACC 986
QY 1061 TGCAACAAACCCGCAAGTCCCAACGTATCCC 1093
Db 987 CTGGACCCACAGCCAAAGTCCCGGATTTATCAC 1019

Search completed: February 7, 2004, 23:31:24
Job time : 532 secs
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: February 7, 2004, 20:53:23 ; Search time 94 Seconds

(without alignments)
6367.186 Million cell updates/sec

Title: US-10-614-954-5

Perfect score: 1356

Sequence: 1 atggcttcaagatacagct.....atggcagtaagttggttag 1356

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

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Issued Patents NA.*

1: /cgn2_6/ptodata/1/ina/5A.COMB.seq.*

2: /cgn2_6/ptodata/1/ina/5B.COMB.seq.*

3: /cgn2_6/ptodata/1/ina/6A.COMB.seq.*

4: /cgn2_6/ptodata/1/ina/6B.COMB.seq.*

5: /cgn2_6/ptodata/1/ina/PCTUS.COMB.seq.*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1356	100.0	1356	4	US-09-538-414-5
2	915.6	67.5	1403	4	US-09-538-414-1
3	915.6	67.5	12949	4	US-09-538-414-11
4	915.6	67.5	13737	4	US-09-538-414-10
5	249.8	18.4	1425	4	US-09-538-414-7
6	39.8	2.9	4403765	3	US-09-103-840A-2
7	39.8	2.9	4411529	3	US-09-103-840A-1
8	34.2	2.5	720	4	US-09-252-991A-16032
9	34.2	2.5	1074	4	US-09-252-991A-16568
10	34.2	2.5	2721	4	US-09-252-991A-16144
11	33.4	2.5	516	4	US-09-252-991A-15293
12	33.4	2.5	1614	4	US-09-252-991A-15438
13	32.8	2.4	1230025	4	US-09-198-452A-1
14	32.4	2.4	1620	4	US-09-125-642C-9
15	32.4	2.4	1740	4	US-09-125-642C-2
16	32.4	2.4	1742	4	US-09-125-642C-13
17	32.4	2.4	5515	4	US-09-125-642C-8
18	32.4	2.4	5519	4	US-09-125-642C-12
19	32.2	2.4	1482	4	US-09-252-991A-8923
20	32.2	2.4	1782	4	US-09-252-991A-9072
21	32.2	2.4	2121	4	US-09-252-991A-9159
22	32	2.4	1406	4	US-09-699-266A-10
23	31.4	2.3	1482	4	US-09-252-991A-1338
24	31.4	2.3	1671	4	US-09-252-991A-1222
25	31.4	2.3	1917	4	US-09-252-991A-1386
26	31.4	2.3	2190	2	US-08-492-027A-7
27	31.2	2.3	456	4	US-09-252-991A-6665

C	28	31.2	2.3	480	4	US-09-410-551B-64	Sequence 64, Appl
C	29	31.2	2.3	1611	4	US-09-252-991A-6694	Sequence 6694, Ap
C	30	31.2	2.3	2577	4	US-09-252-991A-6607	Sequence 6607, Ap
C	31	31.2	2.3	4466	4	US-09-410-551B-20	Sequence 20, Appl
C	32	31.2	2.3	9862	4	US-09-691-861A-3	Sequence 3, Appli
C	33	31.2	2.3	77536	4	US-09-410-551B-1	Sequence 1, Appli
C	34	31	2.3	5183	1	US-08-459-568-3	Sequence 3, Appli
C	35	31	2.3	5183	2	US-08-399-411-3	Sequence 3, Appli
C	36	31	2.3	5467	2	US-08-605-106-7	Sequence 3, Appli
C	37	31	2.3	5868	3	US-08-516-859A-3	Sequence 7, Appli
C	38	31	2.3	5868	4	US-09-586-472-3	Sequence 3, Appli
C	39	31	2.3	5868	4	US-09-528-706-3	Sequence 3, Appli
C	40	30.6	2.3	1263	4	US-09-252-991A-10039	Sequence 10039, A
C	41	30.6	2.3	1353	4	US-09-252-991A-9985	Sequence 9985, Ap
C	42	30.6	2.3	1569	4	US-09-252-991A-9806	Sequence 9806, Ap
C	43	30.4	2.2	480	4	US-09-410-551B-68	Sequence 68, Appl
C	44	30.4	2.2	1710	4	US-09-252-991A-7942	Sequence 7942, Ap
C	45	30.4	2.2	2718	4	US-09-252-991A-7538	Sequence 7538, Ap

ALIGNMENTS

RESULT 1
US-09-538-414-5
; Sequence 5, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 1356
; TYPE: DNA
; ORGANISM: Fusarium graminearum
US-09-538-414-5

Query Match	100.0%;	Score 1356;	DB 4;	Length 1356;	
Best Local Similarity	100.0%;	Pred. No. 0;			
Matches 1356;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;	
QY	1	ATGGCTTTCAAGATACAGCTTCGACACCTCGGCCAGCTACCGAGCCCTCCTTTTCGATCTAC	60		
Db	1	ATGGCTTTCAAGATACAGCTTCGACACCTCGGCCAGCTACCGAGCCCTCCTTTTCGATCTAC	60		
QY	61	ACCCAATCAGTCTCCTCTACCCCGTCTCTGATTCCTCAATATCCCACTATTGTTCAGC	120		
Db	61	ACCCAATCAGTCTCCTCTACCCCGTCTCTGATTCCTCAATATCCCACTATTGTTCAGC	120		
QY	121	ACCTTCGAGCAAGGCTCTTAAGCGCTTCTCGAAGCGGTCCCATGGTGGTCGAGGCCAGGTC	180		
Db	121	ACCTTCGAGCAAGGCTCTTAAGCGCTTCTCGAAGCGGTCCCATGGTGGTCGAGGCCAGGTC	180		
QY	181	AAAGCCGAGGCGATTAGCGAGGGAACACAGGGAACCTTCCTTTATCGTCCCTTTTGAGGAC	240		
Db	181	AAAGCCGAGGCGATTAGCGAGGGAACACAGGGAACCTTCCTTTATCGTCCCTTTTGAGGAC	240		
QY	241	GTTCTCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGCGGCCACGATCGAGGGT	300		
Db	241	GTTCTCTCGTGTGTAGTGAAGACCTTCGCGATGATCTTCAGCGGCCACGATCGAGGGT	300		
QY	301	ATGAGAAGCGGGATACCCCTATGGCGATGTTTGACGAGAAACATCATCGCGCCAAGGAAG	360		

301 ATGGAAGGCGGTACCCCTATGGCGATGTTTTCAGAGAACATCATCGCGCAAGGAAG 360
Db
361 AGTTACCTATTGGACCTGGTACTGGTCCGAGGACCCGAAAGCCTCTTAATTCATTGCGAG 420
QY
361 AGTTACCTATTGGACCTGGTACTGGTCCGAGGACCCGAAAGCCTCTTAATTCATTGCGAG 420
Db
421 CTCACCTTCATCAAGGGCGGACTCATCTCTCACTGTCAACGGACAGACGCTGTATGGAT 480
QY
421 CTCACCTTCATCAAGGGCGGACTCATCTCTCACTGTCAACGGACAGACGCTGTATGGAT 480
Db
481 ATGGTAGGCAAGATCGCGGTATCCGTTCTACTCTCAAGCGCGTCCGTAACGACCCATTC 540
QY
481 ATGGTAGGCAAGATCGCGGTATCCGTTCTACTCTCAAGCGCGTCCGTAACGACCCATTC 540
Db
541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 600
QY
541 ACCGAAGAGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAA 600
Db
601 AACTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGGTGGT 660
QY
601 AACTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGGTGGT 660
Db
661 GACGCTGTTCTACGCGCGGTCACTGCAAGCTGGCGGTTCTTCAATTCAGCCCAAGGCC 720
QY
661 GACGCTGTTCTACGCGCGGTCACTGCAAGCTGGCGGTTCTTCAATTCAGCCCAAGGCC 720
Db
721 ATGTGAGAGTCAAGGATGTCTACCAAGACTCTTGAAGCTGATCAAGAGTTCTGCTGTCG 780
QY
721 ATGTGAGAGTCAAGGATGTCTACCAAGACTCTTGAAGCTGATCAAGAGTTCTGCTGTCG 780
Db
781 ACTGAGCATGCTCTTTCGGGCTTCATCTGGAATTCGGGCTCTCGCGTCTCGAAGA 840
QY
781 ACTGAGCATGCTCTTTCGGGCTTCATCTGGAATTCGGGCTCTCGCGTCTCGAAGA 840
Db
841 ATCGATGGCTCTGCACCTACCGAGTCTGCGGCTGCTGTTGATGCTGACCGGCAATGGT 900
QY
841 ATCGATGGCTCTGCACCTACCGAGTCTGCGGCTGCTGTTGATGCTGACCGGCAATGGT 900
Db
901 GTCTCGAACAATACCGAGCCTCTTCAAAAATGACCTACCAACTCGACCATCGGC 960
QY
901 GTCTCGAACAATACCGAGCCTCTTCAAAAATGACCTACCAACTCGACCATCGGC 960
Db
961 GAAATGCCAACAGTCACTCGCGCAACAGAGCTACGCGCTTCGTTGAGAACTCGACCCC 1020
QY
961 GAAATGCCAACAGTCACTCGCGCAACAGAGCTACGCGCTTCGTTGAGAACTCGACCCC 1020
Db
1021 GCGAGCATGCGCGAGCAACAGAGTCTCGCGAGCTACCTGCAACAACCCCGACAAG 1080
QY
1021 GCGAGCATGCGCGAGCAACAGAGTCTCGCGAGCTACCTGCAACAACCCCGACAAG 1080
Db
1081 TCCAAAGTATCCCTGACGGCTGATGCGGACCCATCTACGAGCTGATGCTGAGTCTTGG 1140
QY
1081 TCCAAAGTATCCCTGACGGCTGATGCGGACCCATCTACGAGCTGATGCTGAGTCTTGG 1140
Db
1141 GCGAAGTGGGACTCTGGGATTACGCTTTGGGCTCGGACTGCGGTAAAGCCGAGACTGTG 1200
QY
1141 GCGAAGTGGGACTCTGGGATTACGCTTTGGGCTCGGACTGCGGTAAAGCCGAGACTGTG 1200
Db
1201 AGACGGCCAACTTTTGAAGCCTGTTGAGAGCTGTGATGTAATTTGCCCCAAGACCTGAT 1260
QY
1201 AGACGGCCAACTTTTGAAGCCTGTTGAGAGCTGTGATGTAATTTGCCCCAAGACCTGAT 1260
Db
1261 GCGAGTTCGTGGCGGCTTCTCTGAGGATGAGGATGAGCCGATGAGCCGATGAGCCGAT 1320
QY
1261 GCGAGTTCGTGGCGGCTTCTCTGAGGATGAGGATGAGCCGATGAGCCGATGAGCCGAT 1320
Db
1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
QY
1321 AAGGAGTGGACCAAGTATGCGCAGTACGTTGGTTAG 1356
Db

RESULT 2

US-09-538-414-1

/ Sequence 1, Application US/09538414
/ Patent No. 6346655
/ GENERAL INFORMATION:
/ APPLICANT: Hohn, T.
/ APPLICANT: Salmeron, J.
/ APPLICANT: Peters, C.
/ APPLICANT: Kendra, D.
/ APPLICANT: Reinders, J.
/ APPLICANT: Kuznia, R.
/ APPLICANT: Dill-Mackey, R.
/ TITLE OF INVENTION: Transgenic Plant and Methods
/ FILE REFERENCE: sequence list
/ CURRENT APPLICATION NUMBER: US/09/538,414
/ CURRENT FILING DATE: 2000-03-29
/ NUMBER OF SEQ ID NOS: 11
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 1403
/ TYPE: DNA
/ ORGANISM: Fusarium sporotrichioides
US-09-538-414-1

Query Match 67.5%; Score 915.6; DB 4; Length 1403;
Best Local Similarity 80.3%; Pred. No. 3.9e-282;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GGCTTTCAAGATACAGCTCGACACCTCGGCCAGCTACCAAGGCTCTCTTCGATCTACAC 62
Db 36 GTCTTTTGACATAGAGCTCGACATCATCGGCCAGCAACGCGCTCTCTTCAATCTACAC 95
QY 63 CCAAAATCAGTCTCTTACCCCGTCTGATTCCTCTCAATATCCACATTTCTCAGCAC 122
Db 96 CCAGATCAGTCTCGTTTACCCCGTCTGATTCCTCCAGTATCCCAACCATCGTCAGCAC 155
QY 123 CTTTCGAGCAGCTTTAAGCGCTTCTCCGAAGCGCTCCCATGGTCCGAGCCAGGCTCAA 182
Db 156 CTTTGAAGAAAGGCTTAAACGCGCTCTCTCAAACTTCCCATGGGTCCGGGCCAGGCTCAA 215
QY 183 AGCCGAGGCGATTAGCGAGGGAACAACAGGAACCTTCTTTATCGTCCCTTTTGAAGACGT 242
Db 216 GACGAGGCGATCAGCGAAGAAACAACAGGAACCTTCCAGATCATTCATATAGGAGAC 275
QY 243 TCCTCGTGTGTAGTGAAAGACCTCCCGATGATTCCTTCAAGGCCACGATCGAGGCTAT 302
Db 276 ACCCGTCTTGTGTGAAAGACCTCCCGTGTATTCCTCAGCGCCAAACGATCGAGGGGT 335
QY 303 GAGAAAGCGGGATACCTTATGGGATGTTGAGGAGAACATCATCGCCCAAGGAAGAC 362
Db 336 GAGAAAGCGGGTTTCCCTTTAGAGATGTTTGAAGAGAACGTCGTCGCTCGAGAGAGAC 395
QY 363 GTTACCTATTGGACCTGTACTGTCCCGACGACCCAAAGCCTGTAAATCTTATTCGAGCT 422
Db 396 ATTAGCTATCGACCTGGCATGGCCCAACGACCCGAGGCTGTGTGCTATTGCGAGCT 455
QY 423 CAATCTCATCAAGGCGGAGCTCATCTCATCTGTCAACGAGCAGACGCTGTATGGATAT 482
Db 456 CAATCTCATTAAGGCGGAGCTCATCTCATCGCTCAACGAGCAACATGCTGTATGGACAT 515
QY 483 GGTAGGCAAGATGCGGTGATTCGCTTCTTCAAGCGGTGCGGTAAACCCCATTCAC 542
Db 516 GACAGCAAGATGCAATTAATTCGCTCTTCTCCAGCGGTGCGGCAACGATCATTCAC 575
QY 543 CGAAGAGAAATGACGCGCATGAACCTCGATCGCAAGACGATAGTTCCTTACCTTGAAGA 602
Db 576 CGAGAGGAATCTCGGCCATGAACCTCGATCGCAAGACGCTAGTTCCTTCTCTTGAAGA 635
QY 603 CTATACGATTGGCCCGGAGGTAGATCATCAGATTGTCAAAGCTGATGTAGTGTGGTGA 662
Db 636 CTACAAAGTTGGTCTCGAGCTAGACCAACGATCGCAAAACCC---TGCCTGCTGTGGCGA 692
QY 663 CGCTGTTCTCACGCGGTCAGTGCAAGCTGGCGGTCTTTCATTCAGCCCCCAAGGCCAT 722
Db 693 CGCTCCACCCGACCGGCCAAGGCAAGCTGGGCGGTTCTTTTCATTCATCCCAAGGCCCT 752

QY 1083 CAACTATCCCTGACGGCTGATCGGACCCATCTACAGCGTCATGCTGAGTCTTTGGGC 1142
DB 12358 GAGCGTCTCCCTGACCGCGATCGGATCCGTCAGCAGATCATGCTGAGTCTTGGGC 12417
QY 1143 CAAAGTGGGACTCTGGGATTAAGACTTTGGGCTCGGACTGGGTAAGCCCGAGACTGTGAG 1202
DB 12418 CAAAGTGGGATGCTGGGATATGACTTTGGGTTGGACTGGGTAAGCCCTGAGAGTGTGAG 12477
QY 1203 AGCGCAATCTTTGAGCCCTGTTGAGAGCTGTGATGTAATTTAGCCCAAGAGCCCTGATGG 1262
DB 12478 AAGACCTCGCTTTGAACCTTTTGGAGAGTTTGTATGTAATTTATGCCCCAAGAGCCCTGATGG 12537
QY 1263 CGAGTTCTGTGGCGCTTCTCTGAGGGATGAGGATATGAGCCGATTTGAAGCGGATAA 1322
DB 12538 GGAGTTTACGGCTCCATTTCTCTGAGGGATGAGGATATGAGAGACTAAAGCGGATGA 12597
QY 1323 GGAGTGGACCAAGTATCGGAGTACGTTGGTTAG 1356
DB 12598 GGAGTGGACCAAGTACGCAAGTATATTTGGGTAG 12631

RESULT 4
US-09-538-414-10
; Sequence 10, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: Patentin ver. 2.0
; SEQ ID NO 10
; LENGTH: 13737
; TYPE: DNA
; ORGANISM: Plasmid
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Plasmid
US-09-538-414-10

Query Match 67.5%; Score 915.6; DB 4; Length 13737;
Best Local Similarity 80.3%; Pred. No. 1.3e-281;
Matches 1087; Conservative 0; Mismatches 264; Indels 3; Gaps 1;

QY 3 GCGTTTCAAGATACAGCTCGACACCCCTCGGCGAGCTACAGGCTCCTTTGATCTACAC 62
DB 50 GTCTTTTGACATAGAGTCGACATCATCGGCAGCAACCGCTCTCTTTTCAATCTACAC 109
QY 63 CCAATCAGTCTCTCTACCCGCTCTGATCTCTCAATATCCCACTATTGTGAGCAGC 122
DB 110 CCAGATCAGTCTCTGTTTACCCGCTCTGATCCCTCCAGTATCCCACTCTGTCAGCAGC 169
QY 123 CTTTCAGCAGAGTCTTAAGCGCTTCTCCGAGCGCTGCCATGGGTCCGAGCCAGGTCAA 182
DB 170 CTTTGGAGAGGCCCTAAACGCTCTCTCAAACTTCCCATGGGTCCGCGGCCAGGTCAA 229
QY 183 AGCCGAGGCAATGAGGAGGAAACACAGAACTTCTTTATCGTCCCTTTTGGAGGAGT 242
DB 230 GACCGAGGCAATGAGGAGGAAACACAGAACTTCCAAAGTATCCATATGAGGAGAC 289
QY 243 TCCTCGTCTTGTAGTGAAGACCTCCGAGTATGCTTCCAGCGCCACGATCGAGGATAT 302
DB 290 ACCCGCTCTGTGTGAAGACCTCCCGTGATTCCTCAGCGCCAAAGATCGAGGGTT 349
QY 303 GAGAAAGCGGGATACCCCTATGGGATGTTTTCAGAGCAACATCATCGGCCCAAGGAAGAC 362

DB 350 GAGAAAGCGCGGTTTCCCTTAGAGATGTTTGAAGAAACGTCGTCCTCCGAGGAAGAC 409
QY 363 GTTACCTATTGGACCTGGTACTGGTCCCGACGACCCAAAGACCTGTAAATTTCTATTGAGCT 422
DB 410 ATTAGCTATCGGACCTGGCAATGGCCCAACGACCCGAGGCTGTGTGCTATTGAGCT 469
QY 423 CAACTTTCATCAAGGGCGGACTCATCTCTCACTGTCTCAACGAGCAGCAGGTCGTCTATGATAT 482
DB 470 CAACTTTCATTAAGGGCGGACTCATCTCTCAACCGTCAACGAGCAACATGGTCTATGAGCAT 529
QY 483 GGTAGGCAAGATGCGGTGATCGGTCTACTCTCCAGGGGTGCGGTAAAGACCCATTTCAC 542
DB 530 GACAGACAGAATGCAATTAATTCGTTCTCTCAAGGGGTGCGGCAAGCATCATTCAC 589
QY 543 CAAAGAGGAAATGACCGCCATGAACCTCGATCGCAAGACGATAGTTTCTTTACCTTGAATA 602
DB 590 CGAGGAGGAAATCTCGGCCATGNAACCTCGATCGCAAGACGGTAGTCCCTCTCTCTTGAATA 649
QY 603 CTATACGATTTGGCCCGAGGTAGATCATCAGATTGTCAAAGCTGTAGTCTGTGTGTGA 662
DB 650 CTACAAAGTTGGTCTCTGAGCTAGACCAACAGATCGCAAAACC--TGCGCTCTCTGGCGA 706
QY 663 CGCTGTTCTCACGCCCGCTCAGTGAAGCTGGGCGTTCTTTCACATTCAGCCCCCAAGGCCAT 722
DB 707 CGCTCCACCGGCAACCGGCAAGGCAAGCTGGGCGTTCTTTTCAITTCATCTCCCAAGGCCCT 766
QY 723 GTCAGAGCTCAAGGATGCTGTACCAAGACTCTTTGACGATCAACAAAGTTCGTGTGCAG 782
DB 767 CTCGAGCTGAAAGACGACGACCAAAAGACTCTTTGACGGCTCGTCCAAAGTTTGTGTCAAC 826
QY 783 TGACGATGCTCTTTTCGGCGTTTCACTGTGAAATCGGCTCTCGGCTGTGCTCGAAAGAAAT 842
DB 827 TGATGATGCTCTTTTCGGCGTTTATCTGGCAATCAACCTCGCGGTAGCTCTCGCAAGATT 886
QY 843 CGATGCTCTGACCTACCGAGTCTCGGCTGTGTGTGTGATGCTCGACCGGCATTTGGTGT 902
DB 887 GGATGCTTCCACACACTACTGAAATCTTTCGCGCTGTGCAATCGGGGGCCAAATGGCGT 946
QY 903 CTCGAACAACTACCGAGGCTTCTTCAAAACATGACCTACCAACTTCGACCATTCGCGCA 962
DB 947 ATCAAGCATATCCAGGCCCTTCTTCAAAACATGACCTACCATGACTCGACCGTTCGCGA 1006
QY 963 AATCGCCAAAGTCACTCGGCGCAACAGCATCAGCTTTCGTTTCAAGACTCGACCCCGC 1022
DB 1007 AATCGCCAAAGCAACACTTGGCGCAACAGCATCAGCTTCGCTCGGTAACACTCAACAGTGA 1066
QY 1023 GAGATGCGCCAGGACAGAGCTCTCGGAGCTACTCTGACAAACACCCCGCAAGTC 1082
DB 1067 TCGTTTTCGCGAGACGAAACAAAGCTTTGGCGAGCTATCATGATGGCTGCTGTGACAGTC 1126
QY 1083 CAAAGTATCCCTGACGGCTGATCGGACCCATCTTACCGAGCTCATGTGAGTCTTGGGC 1142
DB 1127 GAGGCTCTCTGACCGCGCATGCGATCCGTCAAGCAGCATCATGTGAGTCTTGGGC 1186
QY 1143 CAAAGTGGGACTCTGGGATTAAGACTTTGGGCTCGGCTCGGCTGAGGTCGAGCTGTGAG 1202
DB 1187 CAAAGTGGGATGCTGGGAGTATGACTTTGGGTTTGGACTGGTGAAGCTCGAGCTGTGAG 1246
QY 1203 ACGGCCAATCTTTGAGCTCTGTGAGCTTCACTGTTATGCTCCCAAGAGCCCTGTAGG 1262
DB 1247 AAGACCTCGCTTTGAACCTTTTGAAGTTTGAATGATCTTTATGCCCCAAGAGCCCTGTAG 1306
QY 1263 CGAGTCTGTGGCGGCTTTCTCTGAGGATGAGGATATGAGCATGAGCCGATTTGAAGGGCGATAA 1322
DB 1307 GGAGTTTACGGCTTCCATTTCTCTGAGGATGAGGATGAGGATGAGGAGACTTAAAGCGGATGA 1366
QY 1323 GGAGTGAACCAAGTATGCGAGTACGTTGGTTAG 1356
DB 1367 GGAGTGAACCAAGTACGCAAAAGTATATTGGGTAG 1400

RESULT 5
US-09-538-414-7

; Sequence 7, Application US/09538414
; Patent No. 6346655
; GENERAL INFORMATION:
; APPLICANT: Hohn, T.
; APPLICANT: Salmeron, J.
; APPLICANT: Peters, C.
; APPLICANT: Kendra, D.
; APPLICANT: Reinders, J.
; APPLICANT: Kuznia, R.
; APPLICANT: Dill-Mackey, R.
; TITLE OF INVENTION: Transgenic Plant and Methods
; FILE REFERENCE: sequencelist
; CURRENT APPLICATION NUMBER: US/09/538,414
; CURRENT FILING DATE: 2000-03-29
; NUMBER OF SEQ ID NOS: 11
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 7
; LENGTH: 1425
; TYPE: DNA
; ORGANISM: Saccharomyces cerevisiae
US-09-538-414-7

Query Match 18.4%; Score 249.8; DB 4; Length 1425;
Best Local Similarity 51.9%; Pred. No. 1.5e-69;
Matches 700; Conservative 0; Mismatches 622; Indels 27; Gaps 5;

QY 16 CAGCTGACACCTCGGCGACCTGACAGGCTCTCTTTCGATCTACACCAAATCAGTCTC 75
Db 64 CAACCTGATATTTTGGGACAAACCTTCGCTATACAACTATACACTCAATATGCTCT 123

QY 76 CTCTACCCCGTCTCTGATTCCTCTCAATATCCACTATTGTCAGCAGCTTCGACAGGT 135
Db 124 ATCTACCGTGTACAGATCTCTTCTGCTCATGACCATATCGTAATACCTTAAACAGGGA 183

QY 136 CTTAAGCGCTTCTCCGAGCGCTCCCATGCGTTCGAGGCCAGGTCAAAGCCGAGGGCAT 195
Db 184 CTTGAACATTTGGCTAAATAATTTCCAGTGGCTAGCAGGAATGCTGTAATGAGGTCT 243

QY 196 AGCAGGGAACACAGAACTCTCTTATCTGCTCTGCTTTGAGGAGCTTCCTGCTGTTGA 255
Db 244 GACGAAGCTAACACTGCTGCTACAGAAATTTGCGCGTCAGACAAAATCCAC---TTATC 300

QY 256 GTGAAGACCTCCGCGATGATCTTTCAGCGCCACAGATCAGAGGTATCAGAAAGCGGGA 315
Db 301 GTCCAGATCTTCAGAGATCTCTGTCGCCCAACAAATGGAATTCGTTGAAAAGCTGAC 360

QY 316 TACCTATGCGATGTTTGGAGAGAACATCATCGCGCCCAAGAAAGAGCTT-----ACCT 369
Db 361 TTTCTATCTACATGTTAGAGAAAGACTTTTGGCGCTTGCATGACTATCAATCCACCT 420

QY 370 ATTGGACCTGTTGTCGCGAGCAGCCAAAGCTCTTAATCTTATTCGAGCTCAACTTC 429
Db 421 GGAACACTATAGGTATGCGCGCCCAAGAGTGGGCTGTATTTCAGATTCAAGCAAACTTT 480

QY 430 ATCAAGCGCGACTCATCTCTCAGTCAACGAGCAGCAGCTGCTATGATATGATAGGC 489
Db 481 ATCTCCGGCGGCTCTGCTTAATCTTTCGCGCAGCAATATATGATATACAGGA 540

QY 490 CAGATCGGTGATCCGCTCTACTCTCAAGCGTGCAGTCAACGCCCACTCACCGAAGAG 549
Db 541 CAGAAAGTATCATCAACTGCTCAATTAATCTTGGCCACCAAAACCTTCTCTGATGA 600

QY 550 GAAATGCGGCATGAACCTCGATCGCAAGAGATGTTCTTACCTTGAAATATATACG 609
Db 601 GAACCTGCTATGGAATATAGATAAAAGCAAACTATCTCTTTGTTGATGAACTTG 660

QY 610 ATT---GGCCCGAGGTAGATCATCATGTTCAAGCTGATGATGCTGGTGGTGCCT 666
Db 661 GAACCCGACACCGCTAGTGTATGTAATAGTGAACCTCTAGAAATACAGAGTGGAG 720

QY 667 GTTCTCAGCGCGTTCAGT-----GCAAGCTGGGCGTCTCTCACTATCAGCCCAAG 717
Db 721 GAAAGGAACAGTCTTCTTCTGAACTCTACTTTGGGCTTATGTTGAATTTCTGCTATC 780

QY 718 GCCATGTCAGAGCTCAAGGATGCTGCTACCAAGACTCTTGACGATCAACAAGTTCTG 777
Db 781 TCAUTGCAGAACTCTCAGGATTTTGGCAATGACAGATGCTACTTCTGGCACAATAATTTGTC 840

QY 778 TCGACTGACGATGCTCTTTTCGGGCTTCACTCTGGAATCGGCTCTCGGGTGGTCTCGAA 837
Db 841 TCCACTGATGATATGCTGCTCACTGCTTTCACTCTGGAATCAGTTTCTCGAGCCCGTTTCT 900

QY 838 AGAATCGATGCTCTGCACTACCGAGTCTCGCGTCTGCTGCTGCTCGACCGCAATG 897
Db 901 CGACTTAAACAGAAACGAAATCAATTTAGGGCTGCTGGAATGTTAGAAACCGGTA 960

QY 898 GGTGCTCGAAACAATCCAGGCTCTTCAAAACATGACCTACCAACCTCGACCATC 957
Db 961 GGAATCCCGGAAAGCTATCCAGGCTTATTAGTCAACATGACCTTTAATACAGGTTCCCTG 1020

QY 958 GGCAGAAATCGCAACGAGTCACTCGGCGCAACAGCATCACGCTTCTGTCAGACTCGAC 1017
Db 1021 AAAAGCTTGGATCATATAAAGTTTGGGCGTCTTGCATCACAGATTCGAGGAAGCTAGAC 1080

QY 1018 CCCGCGAGCA-----TGCGCCAGCAACAGAGTCTCGCGAGTACTCTGCACAACAAC 1071
Db 1081 CCTAAGCTCTCGATTTGGCCTATATACATGCGACTTGTAGCTCTCTTAGCGATGC 1140

QY 1072 CCCGACAGTCCAAAGTATCCCTGACGCTGATGCGGACCATCTACGAGGCTCATGCTG 1131
Db 1141 CCGGACAGACTAAGGTTTCTATACCTCAACCAATTGATATCTTATCTGGAATTTATGCTC 1200

QY 1132 AGTTCTTGGGCAAGTGGGACTCTGGATTAACAATTTGGGCTGCGACTGGTAAAGCCC 1191
Db 1201 AGTTCTGTTGGGCAAGTGGGACTCTGATGACGTTGATTTCAATCTAGGCTTTGGGAAGCCC 1260

QY 1192 GAGACTGTGAGAGCGCAATCTTTGAGCTCTTCAGAGCTGATGCTACTTTATGCCCAAG 1251
Db 1261 AAGAGTGTACGACGCGCGCTTCATTTCCCTGAGGCTTAATATTTATGCTTGA 1320

QY 1252 AAGCTGATGCGAGTCTCTGCGGCGCTTTCTCTGAGGATGAGGATGACCGGATTG 1311
Db 1321 TCTTCCAGAGTGAATGGTGTGCTCTTTGCTTAGAGATAAGATTTGGAGTGGCTG 1380

QY 1312 AAGCGGATGAGGATGACCAAGTATGC 1340
Db 1381 AATCGGATAAAGAATGACAAATTAATGC 1409

RESULT 6

US-09-103-840A-2
; Sequence 2, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 4403765
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; FEATURE:
; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2

Query Match 2.9%; Score 39.8; DB 3; Length 4403765;

Best Local Similarity 49.8%; Pred. No. 1.3; Mismatches 102; Indels 0; Gaps 0;
Matches 101; Conservative 0;
QY 956 TCGGCGAAATCCCAACGAGTCACTCGCGCGCAACAGCATATCGCTTCGTTCAGAACTCG 1015
Db 4219416 TCGAGGAGTTTCGGCGCGCCCACTCGAAGAGCCAGCGCAATCGCTACGCGATATCC 4219475
QY 1016 ACCCGCGAGATGCGCCAGCGAACAAGAGGTCTCGGAGCTACCTGCAACAACCCCG 1075
Db 4219476 ACGCCACAGCATCCGCAACTCGAAGATGGTCTGGCCCCGGAACCTGCGGAGAGCTCG 4219535
QY 1076 ACAAGTCCAACTATCCCTGACGGCTGATCGCGACCCATCTACACGCGTCATCTGAGTT 1135
Db 4219536 ACGGCTTACCTGCGCTTCAACAGAGACGCCCTCGGAGCGGATTCGGCATTCG 4219595
QY 1136 CTTGGGCCAAGTGGGACTCTGG 1158
Db 4219596 CCGAGGCACAGCTGGTGGGCTGG 4219618

RESULT 7
US-09-103-840A-1
; Sequence 1, Application US/09103840A
; Patent No. 6294328
; GENERAL INFORMATION:
; APPLICANT: FLEISCHMAN, Robert D.
; APPLICANT: WHITE, Owen R.
; APPLICANT: FRASER, Claire M.
; APPLICANT: VENTER, John C.
; TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
; TITLE OF INVENTION: TUBERCULOSIS
; FILE REFERENCE: 24366-20007.00
; CURRENT APPLICATION NUMBER: US/09/103,840A
; CURRENT FILING DATE: 1998-06-24
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 4411529
; TYPE: DNA
; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1

Query Match 2.9%; Score 39.8; DB 3; Length 4411529;
Best Local Similarity 49.8%; Pred. No. 1.3; Mismatches 102; Indels 0; Gaps 0;
Matches 101; Conservative 0;
QY 956 TCGGCGAAATCGCAACGAGTCACTCGCGCGCAACAGCATATCGCGCTTCGTTCAGAACTCG 1015
Db 4227170 TCGAGGAGTTTCGGCGCGCCCACTCGAAGAGCCAGCGCAATCGCTACGGATATCC 4227229
QY 1016 ACCCGCGAGATGCGCGCAGGAAACAGAGGTCTCGGAGCTACTCTGCAACAACCCCG 1075
Db 4227230 ACGCCACAGCATCCGCGAACTCGAAGATGTCTTGGCCCCGGAACCTGCGGAGAGCTCG 4227289
QY 1076 ACAAGTCCAACTATCCCTGACGGCTGATCGGAGCCCATCTACACGCGTCATCTGAGTT 1135
Db 4227290 ACGGCTTACCTGCGCTTCAACAGAGCGCGGTGGCTTCGAGCGCGAGTTGCGCATTCG 4227349
QY 1136 CTTGGGCCAAGTGGGACTCTGG 1158
Db 4227350 CCGAGGCACAGCTGGTGGGCTGG 4227372

RESULT 8
US-09-252-991A-16032
; Sequence 16032, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136

; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16032
; LENGTH: 720
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16032

Query Match 2.5%; Score 34.2; DB 4; Length 720;
Best Local Similarity 53.3%; Pred. No. 0.74; Mismatches 72; Conservative 0; Indels 0; Gaps 0;
QY 474 TATGGATATGTTAGGCCAAGATGCGGTGATCCGTCTACTCTCAAGCGTGCCTTAACGA 533
Db 244 TATGATGCTGGAAGCCAGCAGCGCTGCTTCGGCATCTCGCGAGACAGCCAGGAAGCT 303
QY 534 CCATTCACGAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTA 593
Db 304 CACCATCACCTCGGACGAGATGATGCCATCAGCAACAGGTGACCATGTGCCAGGTC 363
QY 594 CCTTGAATACTATAC 608
Db 364 CCAGGGCGACGAC 378

RESULT 9
US-09-252-991A-16568/c
; Sequence 16568, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16568
; LENGTH: 1074
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16568

Query Match 2.5%; Score 34.2; DB 4; Length 1074;
Best Local Similarity 53.3%; Pred. No. 0.92; Mismatches 72; Conservative 0; Indels 0; Gaps 0;
QY 474 TATGGATATGTTAGGCCAAGATGCGGTGATCCGTCTACTCTCAAGCGTGCCTTAACGA 533
Db 864 TATGATGCTGGAAGCCAGCAGCGCTGCTTCGGCATCTCGCGAGACAGCCAGGAAGCT 805
QY 534 CCATTCACGAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTA 593
Db 804 CACCATCACCTCGGACGAGATGATGCCATCAGCAACAGGTGACCATGTGCGCCAGCTC 745
QY 594 CCTTGAATACTATAC 608
Db 744 CCAGGGCGACGAC 730

RESULT 10
US-09-252-991A-16144
; Sequence 16144, Application US/09252991A
; Patent No. 6551795

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; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 16144
; LENGTH: 2721
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-16144

Query Match          2.5%; Score 34.2; DB 4; Length 2721;
Best Local Similarity 53.3%; Pred. No. 1.5;
Matches 72; Conservative 0; Mismatches 63; Indels 0; Gaps 0;

QY 474 TATGATATGTAGGCCAAGATGCGGTGATCGCTACTCTCCAAGGGTGGCGTAACGA 533
      |||||
Db 1854 TATGATCTGGAAGCCAGCAGCGCTCTTGGCATCTCGCGAGACGCCAGGAAGCT 1913
      |||||

QY 534 CCCATTACCGAAGAGGAAATGACGGCCATGAACCTCGATCGCAAGACGATAGTTCCTTA 593
      |||||
Db 1914 CACCATCACCTCGGACGAGATGAGTGCCATCAGCAACAGGTGAGCCATGTCGCCACGTC 1973
      |||||

QY 594 CTTGAAACTATAC 608
      |||||
Db 1974 CCAGGGGACCAAGAC 1988
      |||||

RESULT 11
US-09-252-991A-15293/c
; Sequence 15293, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15293
; LENGTH: 516
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15293

Query Match          2.5%; Score 33.4; DB 4; Length 516;
Best Local Similarity 52.5%; Pred. No. 1.1;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 896 TGGGTGTCTCGAACAACATACCCAGGCGCTTCTTCAAAACATGACCTACCAACTCGACCA 955
      |||||
Db 187 TGGTTCGGCGCAGGGCCAGGAAATCATTTTGTCTGCACAGGCGGCGCTCGCTCGACAC 128
      |||||

QY 956 TCGGCGAATGCCAACAGATCACTCGGCGCAACAGCATCAGCGCTTCGTTCAAGACTCG 1015
      |||||
Db 127 TGCAGGAAGCCCTGACAGCTCGTGGGCGTGAGGCGCCCGCTCGTCTGCCGAAACGTT 68
      |||||

QY 1016 ACCCGCGCATGCGGCA 1034
      |||||
Db 67 GCGCGAGGCTTGGCGA 49
      |||||
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RESULT 12
US-09-252-991A-15438
; Sequence 15438, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18
; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 15438
; LENGTH: 1614
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-15438

Query Match          2.5%; Score 33.4; DB 4; Length 1614;
Best Local Similarity 52.5%; Pred. No. 2.1;
Matches 73; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 896 TGGGTGTCTCGAACAACATACCCAGGCGCTTCTTCAAAACATGACCTACCAACTCGACCA 955
      |||||
Db 1046 TGGTTCGGCGCAGGGCCAGGAAATCATTTTGTCTGCACAGGCGGCGCTCGCTCGACAC 1105
      |||||

QY 956 TCGGCGAAATCGCAACAGATCACTCGGCGCAACAGCATCAGCGCTTCGTTCAAGACTCG 1015
      |||||
Db 1106 TGCAGGAAGCCCTGCACAGCTCGTGGGCGTGAGGCGCCCGCTCGTCTGCCGAAACGTT 1165
      |||||

QY 1016 ACCCGCGCATGCGGCA 1034
      |||||
Db 1166 GCGCGAGGCGCTTGGCGA 1184
      |||||

RESULT 13
US-09-198-452A-1/c
; Sequence 1, Application US/09198452A
; Patent No. 6559294
; GENERAL INFORMATION:
; APPLICANT: Griffois, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments
; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prevention
; TITLE OF INVENTION: and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
; SEQ ID NO 1
; LENGTH: 1230025
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (1)-(15000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (15001)-(30000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (30001)-(45000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (45001)-(60000)
; OTHER INFORMATION: n=a or c or g or t
; NAME/KEY: misc feature
; LOCATION: (60001)-(75000)
; OTHER INFORMATION: n=a or c or g or t
```



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; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (810001)..(825000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (825001)..(840000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (840001)..(855000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (855001)..(870000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (870001)..(885000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (885001)..(900000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature
; LOCATION: (900001)..(915000)
; OTHER INFORMATION: n-a or c or g or t
; NAME/KEY: misc_feature

Query Match          2.4%; Score 32.8; DB 4; Length 1230025;
Best Local Similarity 59.8%; Pred. No. 98;
Matches 55; Conservative 0; Mismatches 37; Indels 0; Gaps 0;

; 224 TCGTCCCTTTTGAGGACCTCTCTGTTGTAGTGAAGACCTCGCGGATGATCTTCAG 283
Db 772064 TCCCTCCCTTTGACTCTGGAATCTATTGCTATAGCAATGCTTAGCAATCACCTTCAG 772005

; 284 CGCCACATCGAGGTATGAAGAGCGGGA 315
Db 772004 CTGTTACTGCTGGTGGAGGAGATCGGCA 771973

RESULT 14
US-09-125-642C-9
; Sequence 9, Application US/09125642C
; Patent No. 6365393
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
; Their Production and Their Use in Vaccines
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 100 Bayer Road
; CITY: Pittsburgh
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 15205-9741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,642C
; FILING DATE: 20-Aug-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/00729,
; FILING DATE: 17-Feb-97
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1620 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Parapox ovis
; STRAIN: D1701-Proteinkinase-Gen (Version 1)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-125-642C-2

Query Match          2.4%; Score 32.4; DB 4; Length 1620;
Best Local Similarity 46.8%; Pred. No. 4.3;
Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

; ORIGINAL SOURCE:
; ORGANISM: Parapox ovis
; STRAIN: D1701-Proteinkinase-Gen F10L (Version 2)
; SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-125-642C-9

Query Match          2.4%; Score 32.4; DB 4; Length 1620;
Best Local Similarity 46.8%; Pred. No. 4.3;
Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;

Qy 870 CCGTGTCTTTGATGCTCGACCGCAATGGGTGTCTCGAAACAACCTACCCAGGCGCTTCTTCA 929
Db 12 CCATCCCGTTGCTGGCGACTCGGGACTGCCCTCTGTTTTTCTTCCCGTTTCTTCTTAT 71
Qy 930 AAACATGACCTTACCACAACCTCGACCATCGGGGAAATCGCCAAACGAGTCACTGGGCGCAAC 989
Db 72 TAGGTAGTTGTTGCCACCTCCATGATCCTCGCAGCGCTGGCGGGCGACCTCGCACGCC 131
Qy 990 AGCATCAGCGCTTCTGTTTCAGAACTCGACCCCGCGAGCATGCGCCAGCAAGAGGTTCT 1049
Db 132 CGCGCGCGCGCGCGCGCGCGCGCGAGGACGGAAGAACAGTGTATCGCCGGAAGCGCAAGCG 191
Qy 1050 CGCGAGCTTACCTGCAACAACACCCCGCAACGTCCAAACG 1087
Db 192 CAAGACGCCCAACTCGGAAGACGCGCACTCCGACG 229

RESULT 15
US-09-125-642C-2
; Sequence 2, Application US/09125642C
; Patent No. 6365393
; GENERAL INFORMATION:
; APPLICANT: BAYER AG
; TITLE OF INVENTION: Parapoxviruses Which Contain Foreign DNA, and
; Their Production and Their Use in Vaccines
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bayer Corporation
; STREET: 100 Bayer Road
; CITY: Pittsburgh
; STATE: Pennsylvania
; COUNTRY: U.S.A.
; ZIP: 15205-9741
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/125,642C
; FILING DATE: 20-Aug-1998
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: PCT/EP97/00729,
; FILING DATE: 17-Feb-97
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1740 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Parapox ovis
; STRAIN: D1701-Proteinkinase-Gen (Version 1)
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-125-642C-2

Query Match          2.4%; Score 32.4; DB 4; Length 1740;
Best Local Similarity 46.8%; Pred. No. 4.5;
Matches 102; Conservative 0; Mismatches 116; Indels 0; Gaps 0;
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